



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Murphy, Patricia
White, Marga
Olson, Sheri
Yoshikawa, Matthew
Jackson, Geoffrey
Eskanderi, Tara
Schryer, Brenda
Park, Michael
- (ii) TITLE OF THE INVENTION: NOVEL CODING SEQUENCE HAPLOTYPES
OF THE HUMAN BRCA2 GENE
- (iii) NUMBER OF SEQUENCES: 110
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Howrey & Simon
(B) STREET: 1299 Pennsylvania Avenue N.W.
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/084,471
(B) FILING DATE: 22 May 1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Halluin, Albert P
(B) REGISTRATION NUMBER: 25,227
(C) REFERENCE/DOCKET NUMBER: 53710031US02
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-463-8109
(B) TELEFAX: 650-463-8400
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1...50
- (D) OTHER INFORMATION: Exon 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCCTGTTGTT CTACAATGTA CACATGTAAC ACCACAAAGA GATAAGTCAG

50

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1...182
- (D) OTHER INFORMATION: Exon 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATTTAATTAC AAGTCTTCAG AATGCCAGAG ATATACAGGA TATGCGAATT AAGAAGAAAC 60
AAAGGCAACG CGTCTTTCCA CAGCCAGGCA GTCTGTATCT TGCAAAAACA TCCACTCTGC 120
CTCGAATCTC TCTGAAAGCA GCAGTAGGAG GCCAAGTTCC CTCTGCGTGT TCTCATAAAC 180
AG 182

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1...188
- (D) OTHER INFORMATION: Exon 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGTATACGT ATGGCGTTTC TAAACATTGC ATAAAAATTA ACAGCAAAAA TGCAGAGTCT 60
 TTTCAGTTTC AACTGAAGA TTATTTTGGT AAGGAAAGTT TATGGACTGG AAAAGGAATA 120
 CAGTTGGCTG ATGGTGGATG GCTCATACCC TCCAATGATG GAAAGGCTGG AAAAGAAGAA 180
 TTTTATAG 188

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC 60
 TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG 120
 ACAGATTGTG GACCGGCGCG GTTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT 180
 CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT 237
 Met Pro Ile
 1

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC 285
 Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
 5 10 15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT 333
 Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu
 20 25 30 35

TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA 381
 Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu
 40 45 50

CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG 429
 His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg
 55 60 65

AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG 477
 Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu
 70 75 80

CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT 525
 Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp
 85 90 95

AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA 573
 Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys
 100 105 110 115

AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC 621
 Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser
 120 125 130

TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA 669
 Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln
 135 140 145

TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT 717
 Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser
 150 155 160

TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT 765
 Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His
 165 170 175

ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA 813
 Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser
 180 185 190 195

AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC 861
 Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val
 200 205 210

AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT 909
 Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala
 215 220 225

AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT 957
 Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn
 230 235 240

GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA 1005
 Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg
 245 250 255

GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA 1053
 Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys
 260 265 270 275

GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA 1101
 Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu
 280 285 290

GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT 1149
 Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser
 295 300 305

TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA 1197
 Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val
 310 315 320

AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT 1245
 Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp
 325 330 335

GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA 1293

Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr	Ser	Phe	Val	
340					345					350					355	
TCT	GAA	GTG	GAA	CCA	AAT	GAT	ACT	GAT	CCA	TTA	GAT	TCA	AAT	GTA	GCA	1341
Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser	Asn	Val	Ala	
				360					365					370		
CAT	CAG	AAG	CCC	TTT	GAG	AGT	GGA	AGT	GAC	AAA	ATC	TCC	AAG	GAA	GTT	1389
His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser	Lys	Glu	Val	
			375					380					385			
GTA	CCG	TCT	TTG	GCC	TGT	GAA	TGG	TCT	CAA	CTA	ACC	CTT	TCA	GGT	CTA	1437
Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu	Ser	Gly	Leu	
			390					395				400				
AAT	GGA	GCC	CAG	ATG	GAG	AAA	ATA	CCC	CTA	TTG	CAT	ATT	TCT	TCA	TGT	1485
Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile	Ser	Ser	Cys	
	405					410					415					
GAC	CAA	AAT	ATT	TCA	GAA	AAA	GAC	CTA	TTA	GAC	ACA	GAG	AAC	AAA	AGA	1533
Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu	Asn	Lys	Arg	
420					425					430				435		
AAG	AAA	GAT	TTT	CTT	ACT	TCA	GAG	AAT	TCT	TTG	CCA	CGT	ATT	TCT	AGC	1581
Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg	Ile	Ser	Ser	
				440					445					450		
CTA	CCA	AAA	TCA	GAG	AAG	CCA	TTA	AAT	GAG	GAA	ACA	GTG	GTA	AAT	AAG	1629
Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val	Val	Asn	Lys	
			455					460					465			
AGA	GAT	GAA	GAG	CAG	CAT	CTT	GAA	TCT	CAT	ACA	GAC	TGC	ATT	CTT	GCA	1677
Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys	Ile	Leu	Ala	
			470				475					480				
GTA	AAG	CAG	GCA	ATA	TCT	GGA	ACT	TCT	CCA	GTG	GCT	TCT	TCA	TTT	CAG	1725
Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser	Ser	Phe	Gln	
	485					490					495					
GGT	ATC	AAA	AAG	TCT	ATA	TTC	AGA	ATA	AGA	GAA	TCA	CCT	AAA	GAG	ACT	1773
Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro	Lys	Glu	Thr	
500					505					510				515		
TTC	AAT	GCA	AGT	TTT	TCA	GGT	CAT	ATG	ACT	GAT	CCA	AAC	TTT	AAA	AAA	1821
Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn	Phe	Lys	Lys	
				520					525					530		
GAA	ACT	GAA	GCC	TCT	GAA	AGT	GGA	CTG	GAA	ATA	CAT	ACT	GTT	TGC	TCA	1869
Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr	Val	Cys	Ser	
			535					540					545			
CAG	AAG	GAG	GAC	TCC	TTA	TGT	CCA	AAT	TTA	ATT	GAT	AAT	GGA	AGC	TGG	1917
Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn	Gly	Ser	Trp	
			550				555					560				
CCA	GCC	ACC	ACC	ACA	CAG	AAT	TCT	GTA	GCT	TTG	AAG	AAT	GCA	GGT	TTA	1965
Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn	Ala	Gly	Leu	

565 570 575

ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT 2013
 Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His
 580 585 590 595

GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA 2061
 Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser
 600 605 610

GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA 2109
 Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala
 615 620 625

CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG 2157
 Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val
 630 635 640

AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA 2205
 Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu
 645 650 655

ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA 2253
 Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr
 660 665 670 675

TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA 2301
 Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala
 680 685 690

AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT 2349
 Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp
 695 700 705

TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC 2397
 Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser
 710 715 720

AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC 2445
 Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His
 725 730 735

CCA GTA CAA CAT TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC 2493
 Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser
 740 745 750 755

CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA 2541
 Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu
 760 765 770

ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA 2589
 Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg
 775 780 785

GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT 2637
 Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr
 790 795 800

GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA 2685
 Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln
 805 810 815

GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA 2733
 Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro
 820 825 830 835

CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC 2781
 Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe
 840 845 850

AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT 2829
 Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr
 855 860 865

ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC 2877
 Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe
 870 875 880

TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT 2925
 Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn
 885 890 895

AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT 2973
 Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr
 900 905 910 915

TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA 3021
 Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly
 920 925 930

GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG 3069
 Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu
 935 940 945

GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA 3117
 Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile
 950 955 960

AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA 3165
 Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile
 965 970 975

GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA 3213
 Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly
 980 985 990 995

CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA 3261
 Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr
 1000 1005 1010

GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC 3309
 Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser
 1015 1020 1025

AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT 3357
 Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala
 1030 1035 1040

TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG 3405
 Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu
 1045 1050 1055

AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT 3453
 Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser
 1060 1065 1070 1075

GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA 3501
 Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu
 1080 1085 1090

TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA 3549
 Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln
 1095 1100 1105

AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT 3597
 Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser
 1110 1115 1120

CAG TTT GAA TTT ACT CAG TTT AGA AAA CCA AGC TAC ATA TTG CAG AAG 3645
 Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys
 1125 1130 1135

AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT 3693
 Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr
 1140 1145 1150 1155

TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA 3741
 Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro
 1160 1165 1170

TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA 3789
 Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu
 1175 1180 1185

ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT 3837
 Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser
 1190 1195 1200

GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT 3885
 Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe
 1205 1210 1215

TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA 3933
 Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln
 1220 1225 1230 1235

AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT 3981
 Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr
 1240 1245 1250

TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT 4029

Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp
 1255 1260 1265

TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA 4077
 Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val
 1270 1275 1280

AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA 4125
 Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu
 1285 1290 1295

ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA 4173
 Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg
 1300 1305 1310 1315

AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT 4221
 Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser
 1320 1325 1330

CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT 4269
 His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val
 1335 1340 1345

TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC 4317
 Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn
 1350 1355 1360

ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG 4365
 Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln
 1365 1370 1375

ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT 4413
 Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala
 1380 1385 1390 1395

CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT 4461
 Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala
 1400 1405 1410

ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT 4509
 Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe
 1415 1420 1425

TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT 4557
 Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe
 1430 1435 1440

AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC 4605
 Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn
 1445 1450 1455

TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG 4653
 Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met
 1460 1465 1470 1475

GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG 4701
 Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu

1480	1485	1490	
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln 1495 1500 1505			4749
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly 1510 1515 1520			4797
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu 1525 1530 1535			4845
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu 1540 1545 1550 1555			4893
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu 1560 1565 1570			4941
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala 1575 1580 1585			4989
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn 1590 1595 1600			5037
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn 1605 1610 1615			5085
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu 1620 1625 1630 1635			5133
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro 1640 1645 1650			5181
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser 1655 1660 1665			5229
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln 1670 1675 1680			5277
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp 1685 1690 1695			5325
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu 1700 1705 1710 1715			5373

TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT	5421
Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His	
1720 1725 1730	
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC	5469
Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn	
1735 1740 1745	
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC	5517
Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu	
1750 1755 1760	
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT	5565
Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val	
1765 1770 1775	
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA	5613
Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys	
1780 1785 1790 1795	
GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG	5661
Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu	
1800 1805 1810	
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT	5709
Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile	
1815 1820 1825	
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA	5757
Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala	
1830 1835 1840	
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT	5805
Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile	
1845 1850 1855	
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG	5853
Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys	
1860 1865 1870 1875	
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA	5901
Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala	
1880 1885 1890	
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT	5949
Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser	
1895 1900 1905	
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC	5997
Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	
1910 1915 1920	
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG	6045
Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	
1925 1930 1935	

GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA 6093
 Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser
 1940 1945 1950 1955

GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT 6141
 Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser
 1960 1965 1970

GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG 6189
 Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln
 1975 1980 1985

GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA 6237
 Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile
 1990 1995 2000

GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC 6285
 Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn
 2005 2010 2015

GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT 6333
 Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr
 2020 2025 2030 2035

CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT 6381
 Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn
 2040 2045 2050

TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC 6429
 Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser
 2055 2060 2065

ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT 6477
 Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe
 2070 2075 2080

GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA 6525
 Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg
 2085 2090 2095

CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG 6573
 Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu
 2100 2105 2110 2115

CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA 6621
 His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys
 2120 2125 2130

TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC 6669
 Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His
 2135 2140 2145

TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA 6717
 Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln
 2150 2155 2160

CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT 6765

Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val
 2165 2170 2175

TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT 6813
 Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly
 2180 2185 2190 2195

AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT 6861
 Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val
 2200 2205 2210

TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA 6909
 Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala
 2215 2220 2225

GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT 6957
 Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser
 2230 2235 2240

AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT 7005
 Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn
 2245 2250 2255

GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG 7053
 Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu
 2260 2265 2270 2275

CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT 7101
 Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn
 2280 2285 2290

GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA 7149
 Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser
 2295 2300 2305

AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT 7197
 Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His
 2310 2315 2320

CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG 7245
 His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys
 2325 2330 2335

GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA 7293
 Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu
 2340 2345 2350 2355

TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT 7341
 Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser
 2360 2365 2370

TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT 7389
 Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala
 2375 2380 2385

ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC 7437
 Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr

2390 2395 2400

AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT 7485
 Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val
 2405 2410 2415

GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA 7533
 Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln
 2420 2425 2430 2435

AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC 7581
 Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp
 2440 2445 2450

AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT 7629
 Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala
 2455 2460 2465

GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT 7677
 Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser
 2470 2475 2480

CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA 7725
 Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln
 2485 2490 2495

AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA 7773
 Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr
 2500 2505 2510 2515

TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT 7821
 Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val
 2520 2525 2530

CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA 7869
 Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys
 2535 2540 2545

CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC 7917
 His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His
 2550 2555 2560

ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA 7965
 Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile
 2565 2570 2575

CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT 8013
 Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala
 2580 2585 2590 2595

GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT 8061
 Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp
 2600 2605 2610

CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC 8109
 Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile
 2615 2620 2625

ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT 8157
 Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala
 2630 2635 2640

AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA 8205
 Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg
 2645 2650 2655

TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA 8253
 Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile
 2660 2665 2670 2675

ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT 8301
 Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser
 2680 2685 2690

GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA 8349
 Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys
 2695 2700 2705

ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT 8397
 Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp
 2710 2715 2720

GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC 8445
 Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val
 2725 2730 2735

TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA 8493
 Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly
 2740 2745 2750 2755

GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA 8541
 Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro
 2760 2765 2770

GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC 8589
 Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg
 2775 2780 2785

TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG 8637
 Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu
 2790 2795 2800

CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT 8685
 Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp
 2805 2810 2815

GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA 8733
 Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser
 2820 2825 2830 2835

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA 8781
 Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala
 2840 2845 2850

GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT 8829
 Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr
 2855 2860 2865

AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA 8877
 Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro
 2870 2875 2880

TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA 8925
 Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln
 2885 2890 2895

GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT 8973
 Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala
 2900 2905 2910 2915

TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT 9021
 Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn
 2920 2925 2930

CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA 9069
 His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu
 2935 2940 2945

ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA 9117
 Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser
 2950 2955 2960

AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA 9165
 Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys
 2965 2970 2975

AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT 9213
 Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp
 2980 2985 2990 2995

TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT 9261
 Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu
 3000 3005 3010

GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA 9309
 Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu
 3015 3020 3025

GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA 9357
 Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu
 3030 3035 3040

ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA 9405
 Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys
 3045 3050 3055

TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA 9453
 Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile
 3060 3065 3070 3075

GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC 9501

Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val	
3080 3085 3090	
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA	9549
Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile	
3095 3100 3105	
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC	9597
Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser	
3110 3115 3120	
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT	9645
Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe	
3125 3130 3135	
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT	9693
Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe	
3140 3145 3150 3155	
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA	9741
Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile	
3160 3165 3170	
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT	9789
Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn	
3175 3180 3185	
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC	9837
Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr	
3190 3195 3200	
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT	9885
Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser	
3205 3210 3215	
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC	9933
Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala	
3220 3225 3230 3235	
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG	9981
Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys	
3240 3245 3250	
TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG	10029
Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys	
3255 3260 3265	
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT	10077
Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val	
3270 3275 3280	
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG	10125
Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln	
3285 3290 3295	
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA	10173
Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys	

3300 3305 3310 3315

GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT 10221
 Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile
 3320 3325 3330

TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA 10269
 Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile
 3335 3340 3345

AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA 10317
 Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile
 3350 3355 3360

TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT 10365
 Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr
 3365 3370 3375

CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413
 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu
 3380 3385 3390 3395

AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461
 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr
 3400 3405 3410

ATT ACA ACT AAA AAA TAT ATC TAA 10485
 Ile Thr Thr Lys Lys Tyr Ile
 3415

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Pro	Ile	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys
1				5					10					15	
Thr	Arg	Cys	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe
			20					25					30		
Glu	Glu	Leu	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu
			35					40				45			
Glu	Ser	Glu	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr
	50				55					60					
Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile
65				70				75						80	
Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys
			85					90					95		
Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser

Gly	Ser	Trp	Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn
				565					570					575	
Ala	Gly	Leu	Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr
			580					585					590		
Ala	Ile	His	Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp
		595					600					605			
Gln	Lys	Ser	Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala
	610					615					620				
Phe	Glu	Ala	Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His
625					630					635					640
Ser	Ser	Val	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr
				645					650					655	
Leu	Ser	Leu	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg
			660					665					670		
Asn	Glu	Thr	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr
			675				680					685			
Lys	Glu	Ala	Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro
	690					695					700				
Glu	Ala	Asp	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp
705					710					715					720
Pro	Lys	Ser	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala
				725					730					735	
Ala	Cys	His	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp
			740					745					750		
Phe	Gln	Ser	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr
		755					760					765			
Leu	Ile	Leu	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met
	770					775					780				
Ile	Ser	Arg	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly
785					790					795					800
Asn	Asn	Tyr	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu
				805					810					815	
Lys	Asn	Gln	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu
			820					825					830		
Leu	Leu	Pro	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys
		835					840					845			
Val	Gln	Phe	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln
	850					855					860				
Glu	Glu	Thr	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu
865					870					875					880
Glu	Leu	Phe	Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Val	Ala	Asn
				885					890					895	
Glu	Arg	Asn	Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His	Glu	Thr
			900					905					910		
Asp	Leu</														

1010 1015 1020
 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
 1025 1030 1035 104
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
 1045 1050 1055
 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
 1060 1065 1070
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
 1075 1080 1085
 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
 1090 1095 1100
 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
 1105 1110 1115 112
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
 1125 1130 1135
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
 1140 1145 1150
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
 1155 1160 1165
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
 1170 1175 1180
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
 1185 1190 1195 120
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
 1205 1210 1215
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
 1220 1225 1230
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
 1235 1240 1245
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys
 1250 1255 1260
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
 1265 1270 1275 128
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
 1285 1290 1295
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
 1300 1305 1310
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
 1315 1320 1325
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 136
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 144
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
 1460 1465 1470

Asn	Lys	Met	Asp	Ile	Leu	Ser	Tyr	Glu	Glu	Thr	Asp	Ile	Val	Lys	His	1475	1480	1485
Lys	Ile	Leu	Lys	Glu	Ser	Val	Pro	Val	Gly	Thr	Gly	Asn	Gln	Leu	Val	1490	1495	1500
Thr	Phe	Gln	Gly	Gln	Pro	Glu	Arg	Asp	Glu	Lys	Ile	Lys	Glu	Pro	Thr	1505	1510	1515
Leu	Leu	Gly	Phe	His	Thr	Ala	Ser	Gly	Lys	Lys	Val	Lys	Ile	Ala	Lys	1525	1530	1535
Glu	Ser	Leu	Asp	Lys	Val	Lys	Asn	Leu	Phe	Asp	Glu	Lys	Glu	Gln	Gly	1540	1545	1550
Thr	Ser	Glu	Ile	Thr	Ser	Phe	Ser	His	Gln	Trp	Ala	Lys	Thr	Leu	Lys	1555	1560	1565
Tyr	Arg	Glu	Ala	Cys	Lys	Asp	Leu	Glu	Leu	Ala	Cys	Glu	Thr	Ile	Glu	1570	1575	1580
Ile	Thr	Ala	Ala	Pro	Lys	Cys	Lys	Glu	Met	Gln	Asn	Ser	Leu	Asn	Asn	1585	1590	1595
Asp	Lys	Asn	Leu	Val	Ser	Ile	Glu	Thr	Val	Val	Pro	Pro	Lys	Leu	Leu	1605	1610	1615
Ser	Asp	Asn	Leu	Cys	Arg	Gln	Thr	Glu	Asn	Leu	Lys	Thr	Ser	Lys	Ser	1620	1625	1630
Ile	Phe	Leu	Lys	Val	Lys	Val	His	Glu	Asn	Val	Glu	Lys	Glu	Thr	Ala	1635	1640	1645
Lys	Ser	Pro	Ala	Thr	Cys	Tyr	Thr	Asn	Gln	Ser	Pro	Tyr	Ser	Val	Ile	1650	1655	1660
Glu	Asn	Ser	Ala	Leu	Ala	Phe	Tyr	Thr	Ser	Cys	Ser	Arg	Lys	Thr	Ser	1665	1670	1675
Val	Ser	Gln	Thr	Ser	Leu	Leu	Glu	Ala	Lys	Lys	Trp	Leu	Arg	Glu	Gly	1685	1690	1695
Ile	Phe	Asp	Gly	Gln	Pro	Glu	Arg	Ile	Asn	Thr	Ala	Asp	Tyr	Val	Gly	1700	1705	1710
Asn	Tyr	Leu	Tyr	Glu	Asn	Asn	Ser	Asn	Ser	Thr	Ile	Ala	Glu	Asn	Asp	1715	1720	1725
Lys	Asn	His	Leu	Ser	Glu	Lys	Gln	Asp	Thr	Tyr	Leu	Ser	Asn	Ser	Ser	1730	1735	1740
Met	Ser	Asn	Ser	Tyr	Ser	Tyr	His	Ser	Asp	Glu	Val	Tyr	Asn	Asp	Ser	1745	1750	1755
Gly	Tyr	Leu	Ser	Lys	Asn	Lys	Leu	Asp	Ser	Gly	Ile	Glu	Pro	Val	Leu	1765	1770	1775
Lys	Asn	Val	Glu	Asp	Gln	Lys	Asn	Thr	Ser	Phe	Ser	Lys	Val	Ile	Ser	1780	1785	1790
Asn	Val	Lys	Asp	Ala	Asn	Ala	Tyr	Pro	Gln	Thr	Val	Asn	Glu	Asp	Ile	1795	1800	1805
Cys	Val	Glu	Glu	Leu	Val	Thr	Ser	Ser	Ser	Pro	Cys	Lys	Asn	Lys	Asn	1810	1815	1820
Ala	Ala	Ile	Lys	Leu	Ser	Ile	Ser	Asn	Ser	Asn	Asn	Phe	Glu	Val	Gly	1825	1830	1835
Pro	Pro	Ala	Phe	Arg	Ile	Ala	Ser	Gly	Lys	Ile	Val	Cys	Val	Ser	His	1845	1850	1855
Glu	Thr	Ile	Lys	Lys	Val	Lys	Asp	Ile	Phe	Thr	Asp	Ser	Phe	Ser	Lys	1860	1865	1870
Val	Ile	Lys	Glu	Asn	Asn	Glu	Asn	Lys	Ser	Lys	Ile	Cys	Gln	Thr	Lys	1875	1880	1885
Ile	Met	Ala	Gly	Cys	Tyr	Glu	Ala	Leu	Asp	Asp	Ser	Glu	Asp	Ile	Leu	1890	1895	1900
His	Asn	Ser	Leu	Asp	Asn	Asp	Glu	Cys	Ser	Thr	His	Ser	His	Lys	Val	1905	1910	1915
Phe	Ala	Asp	Ile	Gln	Ser	Glu	Glu	Ile	Leu	Gln	His	Asn	Gln	Asn	Met			

1925 1930 1935
 Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
 1940 1945 1950
 Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
 1955 1960 1965
 Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
 1970 1975 1980
 Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
 1985 1990 1995 200
 Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
 2005 2010 2015
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
 2020 2025 2030
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
 2035 2040 2045
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
 2050 2055 2060
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
 2065 2070 2075 208
 Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
 2085 2090 2095
 Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
 2100 2105 2110
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
 2115 2120 2125
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
 2130 2135 2140
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
 2145 2150 2155 216
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
 2165 2170 2175
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
 2180 2185 2190
 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
 2195 2200 2205
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
 2210 2215 2220
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
 2225 2230 2235 224
 Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
 2245 2250 2255
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
 2260 2265 2270
 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
 2275 2280 2285
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
 2290 2295 2300
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
 2305 2310 2315 232
 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
 2325 2330 2335
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
 2340 2345 2350
 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
 2355 2360 2365
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
 2370 2375 2380

Val	Ser	Ala	Thr	Arg	Asn	Glu	Lys	Met	Arg	His	Leu	Ile	Thr	Thr	Gly	2385	2390	2395	240
Arg	Pro	Thr	Lys	Val	Phe	Val	Pro	Pro	Phe	Lys	Thr	Lys	Ser	His	Phe	2405	2410	2415	
His	Arg	Val	Glu	Gln	Cys	Val	Arg	Asn	Ile	Asn	Leu	Glu	Glu	Asn	Arg	2420	2425	2430	
Gln	Lys	Gln	Asn	Ile	Asp	Gly	His	Gly	Ser	Asp	Asp	Ser	Lys	Asn	Lys	2435	2440	2445	
Ile	Asn	Asp	Asn	Glu	Ile	His	Gln	Phe	Asn	Lys	Asn	Asn	Ser	Asn	Gln	2450	2455	2460	
Ala	Ala	Ala	Val	Thr	Phe	Thr	Lys	Cys	Glu	Glu	Glu	Pro	Leu	Asp	Leu	2465	2470	2475	248
Ile	Thr	Ser	Leu	Gln	Asn	Ala	Arg	Asp	Ile	Gln	Asp	Met	Arg	Ile	Lys	2485	2490	2495	
Lys	Lys	Gln	Arg	Gln	Arg	Val	Phe	Pro	Gln	Pro	Gly	Ser	Leu	Tyr	Leu	2500	2505	2510	
Ala	Lys	Thr	Ser	Thr	Leu	Pro	Arg	Ile	Ser	Leu	Lys	Ala	Ala	Val	Gly	2515	2520	2525	
Gly	Gln	Val	Pro	Ser	Ala	Cys	Ser	His	Lys	Gln	Leu	Tyr	Thr	Tyr	Gly	2530	2535	2540	
Val	Ser	Lys	His	Cys	Ile	Lys	Ile	Asn	Ser	Lys	Asn	Ala	Glu	Ser	Phe	2545	2550	2555	256
Gln	Phe	His	Thr	Glu	Asp	Tyr	Phe	Gly	Lys	Glu	Ser	Leu	Trp	Thr	Gly	2565	2570	2575	
Lys	Gly	Ile	Gln	Leu	Ala	Asp	Gly	Gly	Trp	Leu	Ile	Pro	Ser	Asn	Asp	2580	2585	2590	
Gly	Lys	Ala	Gly	Lys	Glu	Glu	Phe	Tyr	Arg	Ala	Leu	Cys	Asp	Thr	Pro	2595	2600	2605	
Gly	Val	Asp	Pro	Lys	Leu	Ile	Ser	Arg	Ile	Trp	Val	Tyr	Asn	His	Tyr	2610	2615	2620	
Arg	Trp	Ile	Ile	Trp	Lys	Leu	Ala	Ala	Met	Glu	Cys	Ala	Phe	Pro	Lys	2625	2630	2635	264
Glu	Phe	Ala	Asn	Arg	Cys	Leu	Ser	Pro	Glu	Arg	Val	Leu	Leu	Gln	Leu	2645	2650	2655	
Lys	Tyr	Arg	Tyr	Asp	Thr	Glu	Ile	Asp	Arg	Ser	Arg	Arg	Ser	Ala	Ile	2660	2665	2670	
Lys	Lys	Ile	Met	Glu	Arg	Asp	Asp	Thr	Ala	Ala	Lys	Thr	Leu	Val	Leu	2675	2680	2685	
Cys	Val	Ser	Asp	Ile	Ile	Ser	Leu	Ser	Ala	Asn	Ile	Ser	Glu	Thr	Ser	2690	2695	2700	
Ser	Asn	Lys	Thr	Ser	Ser	Ala	Asp	Thr	Gln	Lys	Val	Ala	Ile	Ile	Glu	2705	2710	2715	272
Leu	Thr	Asp	Gly	Trp	Tyr	Ala	Val	Lys	Ala	Gln	Leu	Asp	Pro	Pro	Leu	2725	2730	2735	
Leu	Ala	Val	Leu	Lys	Asn	Gly	Arg	Leu	Thr	Val	Gly	Gln	Lys	Ile	Ile	2740	2745	2750	
Leu	His	Gly	Ala	Glu	Leu	Val	Gly	Ser	Pro	Asp	Ala	Cys	Thr	Pro	Leu	2755	2760	2765	
Glu	Ala	Pro	Glu	Ser	Leu	Met	Leu	Lys	Ile	Ser	Ala	Asn	Ser	Thr	Arg	2770	2775	2780	
Pro	Ala	Arg	Trp	Tyr	Thr	Lys	Leu	Gly	Phe	Phe	Pro	Asp	Pro	Arg	Pro	2785	2790	2795	280
Phe	Pro	Leu	Pro	Leu	Ser	Ser	Leu	Phe	Ser	Asp	Gly	Gly	Asn	Val	Gly	2805	2810	2815	
Cys	Val	Asp	Val	Ile	Ile	Gln	Arg	Ala	Tyr	Pro	Ile	Gln	Trp	Met	Glu	2820	2825	2830	
Lys	Thr	Ser	Ser	Gly	Leu	Tyr	Ile	Phe	Arg	Asn	Glu	Arg	Glu	Glu	Glu				

2835 2840 2845
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
 2850 2855 2860
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
 2865 2870 2875 288
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
 2885 2890 2895
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
 2900 2905 2910
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
 2915 2920 2925
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
 2930 2935 2940
 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
 2945 2950 2955 296
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
 2965 2970 2975
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
 2980 2985 2990
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
 2995 3000 3005
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
 3010 3015 3020
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
 3025 3030 3035 304
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
 3045 3050 3055
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
 3060 3065 3070
 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
 3075 3080 3085
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
 3090 3095 3100
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
 3105 3110 3115 312
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
 3125 3130 3135
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
 3140 3145 3150
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
 3155 3160 3165
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
 3170 3175 3180
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
 3185 3190 3195 320
 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
 3205 3210 3215
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
 3220 3225 3230
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
 3235 3240 3245
 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
 3250 3255 3260
 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
 3265 3270 3275 328
 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
 3285 3290 3295

Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
 3300 3305 3310
 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
 3315 3320 3325
 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
 3330 3335 3340
 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
 3345 3350 3355 336
 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser
 3365 3370 3375
 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys
 3380 3385 3390
 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
 3395 3400 3405
 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile
 3410 3415

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 229...10482
 (D) OTHER INFORMATION: BRCA2 (OMI2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGTGGCGCGGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC	60
TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG	120
ACAGATTTGT GACCGGCGCG GTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT	180
CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT	237
Met Pro Ile	
1	
GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC	285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys	
5 10 15	
AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT	333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu	
20 25 30 35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA	381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
40 45 50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
55 60 65	

AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu 70 75 80	477
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp 85 90 95	525
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys 100 105 110 115	573
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser 120 125 130	621
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln 135 140 145	669
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser 150 155 160	717
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His 165 170 175	765
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser 180 185 190 195	813
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val 200 205 210	861
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala 215 220 225	909
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn 230 235 240	957
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg 245 250 255	1005
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys 260 265 270 275	1053
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu 280 285 290	1101
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT	1149

Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser	
295 300 305	
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA	1197
Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val	
310 315 320	
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT	1245
Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp	
325 330 335	
GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA	1293
Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val	
340 345 350 355	
TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA	1341
Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala	
360 365 370	
CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT	1389
His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val	
375 380 385	
GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA	1437
Val Pro Ser Leu Ala Cys Glu Trp Ser Ser Gln Leu Thr Leu Ser Gly Leu	
390 395 400	
AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT	1485
Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys	
405 410 415	
GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA	1533
Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg	
420 425 430 435	
AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC	1581
Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser	
440 445 450	
CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG	1629
Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys	
455 460 465	
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA	1677
Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala	
470 475 480	
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG	1725
Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln	
485 490 495	
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT	1773
Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr	
500 505 510 515	
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA	1821
Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys	

520										525					530					
GAA	ACT	GAA	GCC	TCT	GAA	AGT	GGA	CTG	GAA	ATA	CAT	ACT	GTT	TGC	TCA	1869				
Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr	Val	Cys	Ser					
535					540					545										
CAG	AAG	GAG	GAC	TCC	TTA	TGT	CCA	AAT	TTA	ATT	GAT	AAT	GGA	AGC	TGG	1917				
Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn	Gly	Ser	Trp					
550					555					560										
CCA	GCC	ACC	ACC	ACA	CAG	AAT	TCT	GTA	GCT	TTG	AAG	AAT	GCA	GGT	TTA	1965				
Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn	Ala	Gly	Leu					
565					570					575										
ATA	TCC	ACT	TTG	AAA	AAG	AAA	ACA	AAT	AAG	TTT	ATT	TAT	GCT	ATA	CAT	2013				
Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr	Ala	Ile	His					
580					585					590					595					
GAT	GAA	ACA	TCT	TAT	AAA	GGA	AAA	AAA	ATA	CCG	AAA	GAC	CAA	AAA	TCA	2061				
Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp	Gln	Lys	Ser					
600					605					610										
GAA	CTA	ATT	AAC	TGT	TCA	GCC	CAG	TTT	GAA	GCA	AAT	GCT	TTT	GAA	GCA	2109				
Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala	Phe	Glu	Ala					
615					620					625										
CCA	CTT	ACA	TTT	GCA	AAT	GCT	GAT	TCA	GGT	TTA	TTG	CAT	TCT	TCT	GTG	2157				
Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His	Ser	Ser	Val					
630					635					640										
AAA	AGA	AGC	TGT	TCA	CAG	AAT	GAT	TCT	GAA	GAA	CCA	ACT	TTG	TCC	TTA	2205				
Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr	Leu	Ser	Leu					
645					650					655										
ACT	AGC	TCT	TTT	GGG	ACA	ATT	CTG	AGG	AAA	TGT	TCT	AGA	AAT	GAA	ACA	2253				
Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg	Asn	Glu	Thr					
660					665					670					675					
TGT	TCT	AAT	AAT	ACA	GTA	ATC	TCT	CAG	GAT	CTT	GAT	TAT	AAA	GAA	GCA	2301				
Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr	Lys	Glu	Ala					
680					685					690										
AAA	TGT	AAT	AAG	GAA	AAA	CTA	CAG	TTA	TTT	ATT	ACC	CCA	GAA	GCT	GAT	2349				
Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro	Glu	Ala	Asp					
695					700					705										
TCT	CTG	TCA	TGC	CTG	CAG	GAA	GGA	CAG	TGT	GAA	AAT	GAT	CCA	AAA	AGC	2397				
Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp	Pro	Lys	Ser					
710					715					720										
AAA	AAA	GTT	TCA	GAT	ATA	AAA	GAA	GAG	GTC	TTG	GCT	GCA	GCA	TGT	CAC	2445				
Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala	Ala	Cys	His					
725					730					735										
CCA	GTA	CAA	CAT	TCA	AAA	GTG	GAA	TAC	AGT	GAT	ACT	GAC	TTT	CAA	TCC	2493				
Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp	Phe	Gln	Ser					
740					745					750					755					

CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA	2541
Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu	
760 765 770	
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA	2589
Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg	
775 780 785	
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT	2637
Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr	
790 795 800	
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA	2685
Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln	
805 810 815	
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA	2733
Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro	
820 825 830 835	
CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC	2781
Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe	
840 845 850	
AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT	2829
Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr	
855 860 865	
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC	2877
Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe	
870 875 880	
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT	2925
Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn	
885 890 895	
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT	2973
Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr	
900 905 910 915	
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA	3021
Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly	
920 925 930	
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG	3069
Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu	
935 940 945	
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA	3117
Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile	
950 955 960	
AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA	3165
Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile	
965 970 975	

GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA 3213
 Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly
 980 985 990 995

CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA 3261
 Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr
 1000 1005 1010

GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC 3309
 Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser
 1015 1020 1025

AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT 3357
 Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala
 1030 1035 1040

TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG 3405
 Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu
 1045 1050 1055

AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT 3453
 Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser
 1060 1065 1070 1075

GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA 3501
 Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu
 1080 1085 1090

TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA 3549
 Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln
 1095 1100 1105

AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT 3597
 Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser
 1110 1115 1120

CAG TTT GAA TTT ACT CAG TTT AGA AAR CCA AGC TAC ATA TTG CAG AAG 3645
 Gln Phe Glu Phe Thr Gln Phe Arg Xaa Pro Ser Tyr Ile Leu Gln Lys
 1125 1130 1135

AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT 3693
 Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr
 1140 1145 1150 1155

TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA 3741
 Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro
 1160 1165 1170

TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA 3789
 Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu
 1175 1180 1185

ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT 3837
 Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser
 1190 1195 1200

GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT 3885

Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe	
1205 1210 1215	
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA	3933
Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln	
1220 1225 1230 1235	
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT	3981
Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr	
1240 1245 1250	
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT	4029
Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp	
1255 1260 1265	
TCT GTC GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA	4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val	
1270 1275 1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA	4125
Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu	
1285 1290 1295	
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA	4173
Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg	
1300 1305 1310 1315	
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT	4221
Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser	
1320 1325 1330	
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT	4269
His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val	
1335 1340 1345	
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC	4317
Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn	
1350 1355 1360	
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG	4365
Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln	
1365 1370 1375	
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT	4413
Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala	
1380 1385 1390 1395	
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT	4461
Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala	
1400 1405 1410	
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT	4509
Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe	
1415 1420 1425	
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT	4557
Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe	

1430	1435	1440	
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn 1445 1450 1455			4605
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met 1460 1465 1470 1475			4653
GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu 1480 1485 1490			4701
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln 1495 1500 1505			4749
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly 1510 1515 1520			4797
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu 1525 1530 1535			4845
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu 1540 1545 1550 1555			4893
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu 1560 1565 1570			4941
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala 1575 1580 1585			4989
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn 1590 1595 1600			5037
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn 1605 1610 1615			5085
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu 1620 1625 1630 1635			5133
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro 1640 1645 1650			5181
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser 1655 1660 1665			5229

GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG 5277
 Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln
 1670 1675 1680

ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT 5325
 Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp
 1685 1690 1695

GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG 5373
 Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu
 1700 1705 1710 1715

TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT 5421
 Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His
 1720 1725 1730

CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC 5469
 Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn
 1735 1740 1745

AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC 5517
 Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu
 1750 1755 1760

TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT 5565
 Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val
 1765 1770 1775

GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA 5613
 Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys
 1780 1785 1790 1795

GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG 5661
 Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu
 1800 1805 1810

GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT 5709
 Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile
 1815 1820 1825

AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA 5757
 Lys Leu Ser Ile Ser Asn Ser Asn Phe Glu Val Gly Pro Pro Ala
 1830 1835 1840

TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT 5805
 Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile
 1845 1850 1855

AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG 5853
 Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys
 1860 1865 1870 1875

GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA 5901
 Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala
 1880 1885 1890

GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT	5949
Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser	
1895 1900 1905	
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC	5997
Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	
1910 1915 1920	
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG	6045
Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	
1925 1930 1935	
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA	6093
Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser	
1940 1945 1950 1955	
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT	6141
Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser	
1960 1965 1970	
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG	6189
Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln	
1975 1980 1985	
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA	6237
Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile	
1990 1995 2000	
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC	6285
Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn	
2005 2010 2015	
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT	6333
Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr	
2020 2025 2030 2035	
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT	6381
Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn	
2040 2045 2050	
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC	6429
Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser	
2055 2060 2065	
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT	6477
Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe	
2070 2075 2080	
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA	6525
Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg	
2085 2090 2095	
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG	6573
Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu	
2100 2105 2110 2115	
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA	6621

His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys	
2120 . 2125 2130	
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC	6669
Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His	
2135 2140 2145	
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA	6717
Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln	
2150 2155 2160	
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT	6765
Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val	
2165 2170 2175	
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT	6813
Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly	
2180 2185 2190 2195	
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT	6861
Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val	
2200 2205 2210	
TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA	6909
Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala	
2215 2220 2225	
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT	6957
Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser	
2230 2235 2240	
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT	7005
Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn	
2245 2250 2255	
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG	7053
Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu	
2260 2265 2270 2275	
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT	7101
Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn	
2280 2285 2290	
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA	7149
Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser	
2295 2300 2305	
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT	7197
Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His	
2310 2315 2320	
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG	7245
His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys	
2325 2330 2335	
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA	7293
Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu	

2340	2345	2350	2355	
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT				7341
Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser				
2360	2365	2370		
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT				7389
Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala				
2375	2380	2385		
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC				7437
Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr				
2390	2395	2400		
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT				7485
Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val				
2405	2410	2415		
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA				7533
Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln				
2420	2425	2430	2435	
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC				7581
Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp				
2440	2445	2450		
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT				7629
Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala				
2455	2460	2465		
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT				7677
Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser				
2470	2475	2480		
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA				7725
Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln				
2485	2490	2495		
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA				7773
Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr				
2500	2505	2510	2515	
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT				7821
Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val				
2520	2525	2530		
CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA				7869
Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys				
2535	2540	2545		
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC				7917
His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His				
2550	2555	2560		
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA				7965
Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile				
2565	2570	2575		

CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT 8013
 Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala
 2580 2585 2590 2595

GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT 8061
 Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp
 2600 2605 2610

CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC 8109
 Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile
 2615 2620 2625

ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT 8157
 Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala
 2630 2635 2640

AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA 8205
 Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg
 2645 2650 2655

TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA 8253
 Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile
 2660 2665 2670 2675

ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT 8301
 Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser
 2680 2685 2690

GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA 8349
 Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys
 2695 2700 2705

ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT 8397
 Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp
 2710 2715 2720

GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC 8445
 Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val
 2725 2730 2735

TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA 8493
 Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly
 2740 2745 2750 2755

GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA 8541
 Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro
 2760 2765 2770

GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC 8589
 Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg
 2775 2780 2785

TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG 8637
 Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu
 2790 2795 2800

CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT 8685
Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp
2805 2810 2815

GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA 8733
Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser
2820 2825 2830 2835

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA 8781
Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala
2840 2845 2850

GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT 8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr
2855 2860 2865

AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA 8877
Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro
2870 2875 2880

TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA 8925
Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln
2885 2890 2895

GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT 8973
Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala
2900 2905 2910 2915

TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT 9021
Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn
2920 2925 2930

CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA 9069
His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu
2935 2940 2945

ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA 9117
Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser
2950 2955 2960

AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA 9165
Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys
2965 2970 2975

AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT 9213
Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp
2980 2985 2990 2995

TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT 9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu
3000 3005 3010

GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA 9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu
3015 3020 3025

GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA 9357

Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu
3030 3035 3040

ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA 9405
Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys
3045 3050 3055

TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA 9453
Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile
3060 3065 3070 3075

GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC 9501
Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val
3080 3085 3090

TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA 9549
Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile
3095 3100 3105

GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC 9597
Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser
3110 3115 3120

AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT 9645
Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe
3125 3130 3135

GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT 9693
Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe
3140 3145 3150 3155

CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA 9741
Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile
3160 3165 3170

CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT 9789
Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn
3175 3180 3185

GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC 9837
Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr
3190 3195 3200

ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT 9885
Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser
3205 3210 3215

CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC 9933
Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala
3220 3225 3230 3235

AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG 9981
Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys
3240 3245 3250

TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG 10029
Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys

3255	3260	3265	
AGA AGA GCC TTG GAT TTC TTG AGT	AGA CTG CCT TTA CCT CCA CCT GTT		10077
Arg Arg Ala Leu Asp Phe Leu Ser	Arg Leu Pro Leu Pro Pro Pro Val		
3270	3275	3280	
AGT CCC ATT TGT ACA TTT GTT TCT	CCG GCT GCA CAG AAG GCA TTT CAG		10125
Ser Pro Ile Cys Thr Phe Val Ser	Pro Ala Ala Gln Lys Ala Phe Gln		
3285	3290	3295	
CCA CCA AGG AGT TGT GGC ACC AAA	TAC GAA ACA CCC ATA AAG AAA AAA		10173
Pro Pro Arg Ser Cys Gly Thr Lys	Tyr Glu Thr Pro Ile Lys Lys Lys		
3300	3305	3310	3315
GAA CTG AAT TCT CCT CAG ATG ACT	CCA TTT AAA AAA TTC AAT GAA ATT		10221
Glu Leu Asn Ser Pro Gln Met Thr	Pro Phe Lys Lys Phe Asn Glu Ile		
3320	3325	3330	
TCT CTT TTG GAA AGT AAT TCA ATA	GCT GAC GAA GAA CTT GCA TTG ATA		10269
Ser Leu Leu Glu Ser Asn Ser Ile	Ala Asp Glu Glu Leu Ala Leu Ile		
3335	3340	3345	
AAT ACC CAA GCT CTT TTG TCT GGT	TCA ACA GGA GAA AAA CAA TTT ATA		10317
Asn Thr Gln Ala Leu Leu Ser Gly	Ser Thr Gly Glu Lys Gln Phe Ile		
3350	3355	3360	
TCT GTC AGT GAA TCC ACT AGG ACT	GCT CCC ACC AGT TCA GAA GAT TAT		10365
Ser Val Ser Glu Ser Thr Arg Thr	Ala Pro Thr Ser Ser Glu Asp Tyr		
3365	3370	3375	
CTC AGA CTG AAA CGA CGT TGT ACT	ACA TCT CTG ATC AAA GAA CAG GAG		10413
Leu Arg Leu Lys Arg Arg Cys Thr	Thr Ser Leu Ile Lys Glu Gln Glu		
3380	3385	3390	3395
AGT TCC CAG GCC AGT ACG GAA GAA	TGT GAG AAA AAT AAG CAG GAC ACA		10461
Ser Ser Gln Ala Ser Thr Glu Glu	Cys Glu Lys Asn Lys Gln Asp Thr		
3400	3405	3410	
ATT ACA ACT AAA AAA TAT ATC TAA			10485
Ile Thr Thr Lys Lys Tyr Ile			
3415			

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys

1 5 10 15
 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
 20 25 30
 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
 35 40 45
 Glu Ser Glu His Lys Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
 50 55 60
 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
 65 70 75 80
 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
 85 90 95
 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
 100 105 110
 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
 115 120 125
 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
 130 135 140
 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
 145 150 155 160
 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
 165 170 175
 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
 180 185 190
 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
 195 200 205
 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
 210 215 220
 Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
 225 230 235 240
 Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
 245 250 255
 Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
 260 265 270
 Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
 275 280 285
 Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
 290 295 300
 Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
 305 310 315 320
 Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
 325 330 335
 Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
 340 345 350
 Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
 355 360 365
 Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
 370 375 380
 Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
 385 390 395 400
 Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
 405 410 415
 Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
 420 425 430
 Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
 435 440 445
 Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
 450 455 460

Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
 465 470 475 480
 Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
 485 490 495
 Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
 500 505 510
 Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
 515 520 525
 Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
 530 535 540
 Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
 545 550 555 560
 Gly Ser Trp Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
 565 570 575
 Ala Gly Leu Ile Ser Thr Leu Lys Lys Thr Asn Lys Phe Ile Tyr
 580 585 590
 Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
 595 600 605
 Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
 610 615 620
 Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
 625 630 635 640
 Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
 645 650 655
 Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
 660 665 670
 Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
 675 680 685
 Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
 690 695 700
 Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
 705 710 715 720
 Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
 725 730 735
 Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
 740 745 750
 Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
 755 760 765
 Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
 770 775 780
 Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
 785 790 795 800
 Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
 805 810 815
 Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
 820 825 830
 Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
 835 840 845
 Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
 850 855 860
 Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
 865 870 875 880
 Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
 885 890 895
 Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
 900 905 910
 Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val

915 920 925
 Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
 930 935 940
 Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
 945 950 955 960
 Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
 965 970 975
 Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys
 980 985 990
 Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
 995 1000 1005
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
 1010 1015 1020
 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
 1025 1030 1035 104
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
 1045 1050 1055
 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
 1060 1065 1070
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
 1075 1080 1085
 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
 1090 1095 1100
 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
 1105 1110 1115 112
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Xaa Pro Ser Tyr Ile
 1125 1130 1135
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
 1140 1145 1150
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
 1155 1160 1165
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
 1170 1175 1180
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
 1185 1190 1195 120
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
 1205 1210 1215
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
 1220 1225 1230
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
 1235 1240 1245
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys
 1250 1255 1260
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
 1265 1270 1275 128
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
 1285 1290 1295
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
 1300 1305 1310
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
 1315 1320 1325
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 136
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375

Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 144
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
 1460 1465 1470
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
 1475 1480 1485
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
 1490 1495 1500
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
 1505 1510 1515 152
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
 1525 1530 1535
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
 1540 1545 1550
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
 1555 1560 1565
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
 1570 1575 1580
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
 1585 1590 1595 160
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
 1605 1610 1615
 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
 1620 1625 1630
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
 1635 1640 1645
 Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
 1650 1655 1660
 Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
 1665 1670 1675 168
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
 1685 1690 1695
 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
 1700 1705 1710
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
 1715 1720 1725
 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
 1730 1735 1740
 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
 1745 1750 1755 176
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
 1765 1770 1775
 Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
 1780 1785 1790
 Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
 1795 1800 1805
 Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn
 1810 1815 1820
 Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly

1825 1830 1835 184
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
1845 1850 1855
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
1860 1865 1870
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
1875 1880 1885
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
1890 1895 1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
1905 1910 1915 192
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
1925 1930 1935
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
1940 1945 1950
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
1955 1960 1965
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
1970 1975 1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
1985 1990 1995 200
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
2005 2010 2015
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
2020 2025 2030
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
2035 2040 2045
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
2050 2055 2060
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
2065 2070 2075 208
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
2085 2090 2095
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
2100 2105 2110
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
2115 2120 2125
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
2130 2135 2140
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
2145 2150 2155 216
Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
2165 2170 2175
Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
2180 2185 2190
Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
2195 2200 2205
Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
2210 2215 2220
Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
2225 2230 2235 224
Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
2245 2250 2255
Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
2260 2265 2270
Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
2275 2280 2285

Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
 2290 2295 2300
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
 2305 2310 2315 232
 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
 2325 2330 2335
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
 2340 2345 2350
 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
 2355 2360 2365
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
 2370 2375 2380
 Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
 2385 2390 2395 240
 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
 2405 2410 2415
 His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
 2420 2425 2430
 Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
 2435 2440 2445
 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
 2450 2455 2460
 Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu
 2465 2470 2475 248
 Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
 2485 2490 2495
 Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
 2500 2505 2510
 Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly
 2515 2520 2525
 Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly
 2530 2535 2540
 Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe
 2545 2550 2555 256
 Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly
 2565 2570 2575
 Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp
 2580 2585 2590
 Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro
 2595 2600 2605
 Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr
 2610 2615 2620
 Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys
 2625 2630 2635 264
 Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu
 2645 2650 2655
 Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile
 2660 2665 2670
 Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
 2675 2680 2685
 Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
 2690 2695 2700
 Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
 2705 2710 2715 272
 Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
 2725 2730 2735
 Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile

2740 2745 2750
 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
 2755 2760 2765
 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
 2770 2775 2780
 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
 2785 2790 2795 280
 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
 2805 2810 2815
 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
 2820 2825 2830
 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu
 2835 2840 2845
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
 2850 2855 2860
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
 2865 2870 2875 288
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
 2885 2890 2895
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
 2900 2905 2910
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
 2915 2920 2925
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
 2930 2935 2940
 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
 2945 2950 2955 296
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
 2965 2970 2975
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
 2980 2985 2990
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
 2995 3000 3005
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
 3010 3015 3020
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
 3025 3030 3035 304
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
 3045 3050 3055
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
 3060 3065 3070
 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
 3075 3080 3085
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
 3090 3095 3100
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
 3105 3110 3115 312
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
 3125 3130 3135
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
 3140 3145 3150
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
 3155 3160 3165
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
 3170 3175 3180
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
 3185 3190 3195 320

Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
 3205 3210 3215
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
 3220 3225 3230
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
 3235 3240 3245
 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
 3250 3255 3260
 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
 3265 3270 3275 328
 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
 3285 3290 3295
 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
 3300 3305 3310
 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
 3315 3320 3325
 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
 3330 3335 3340
 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
 3345 3350 3355 336
 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser
 3365 3370 3375
 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys
 3380 3385 3390
 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
 3395 3400 3405
 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile
 3410 3415

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTGGCGCGA	GCTTCTGAAA	CTAGGCGGCA	GAGGCGGAGC	CGCTGTGGCA	CTGCTGCGCC	60
TCTGCTGCGC	CTCGGGTGTC	TTTTGCGGCG	GTGGGTGCGC	GCCGGGAGAA	GCGTGAGGGG	120
ACAGATTTGT	GACCGGCGCG	GTTTTTGTCA	GCTTACTCCG	GCCAAAAAAG	AACTGCACCT	180
CTGGAGCGGA	CTTATTTACC	AAGCATTGGA	GGAATATCGT	AGGTAAAA	ATG CCT ATT	237
					Met Pro Ile	
					1	
GGA TCC AAA	GAG AGG CCA	ACA TTT TTT	GAA ATT TTT	AAG ACA CGC	TGC	285
Gly Ser Lys	Glu Arg Pro	Thr Phe Phe	Glu Ile Phe	Lys Thr Arg	Cys	
5	10		15			

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT	333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu	
20 25 30 35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA	381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
40 45 50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
55 60 65	
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	
70 75 80	
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT	525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	
85 90 95	
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA	573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	
100 105 110 115	
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC	621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	
120 125 130	
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
135 140 145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
150 155 160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
165 170 175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
180 185 190 195	
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
200 205 210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
215 220 225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005

Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr	Asn	Gln	Arg	
245						250					255					
GAA	GCT	GCA	AGT	CAT	GGA	TTT	GGA	AAA	ACA	TCA	GGG	AAT	TCA	TTT	AAA	1053
Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn	Ser	Phe	Lys	
260					265					270					275	
GTA	AAT	AGC	TGC	AAA	GAC	CAC	ATT	GGA	AAG	TCA	ATG	CCA	CAT	GTC	CTA	1101
Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro	His	Val	Leu	
				280					285					290		
GAA	GAT	GAA	GTA	TAT	GAA	ACA	GTT	GTA	GAT	ACC	TCT	GAA	GAA	GAT	AGT	1149
Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu	Glu	Asp	Ser	
			295					300					305			
TTT	TCA	TTA	TGT	TTT	TCT	AAA	TGT	AGA	ACA	AAA	AAT	CTA	CAA	AAA	GTA	1197
Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu	Gln	Lys	Val	
		310					315					320				
AGA	ACT	AGC	AAG	ACT	AGG	AAA	AAA	ATT	TTC	CAT	GAA	GCA	AAC	GCT	GAT	1245
Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala	Asn	Ala	Asp	
			325			330					335					
GAA	TGT	GAA	AAA	TCT	AAA	AAC	CAA	GTG	AAA	GAA	AAA	TAC	TCA	TTT	GTA	1293
Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr	Ser	Phe	Val	
340					345					350					355	
TCT	GAA	GTG	GAA	CCA	AAT	GAT	ACT	GAT	CCA	TTA	GAT	TCA	AAT	GTA	GCA	1341
Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser	Asn	Val	Ala	
				360					365					370		
AAT	CAG	AAG	CCC	TTT	GAG	AGT	GGA	AGT	GAC	AAA	ATC	TCC	AAG	GAA	GTT	1389
Asn	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser	Lys	Glu	Val	
			375					380					385			
GTA	CCG	TCT	TTG	GCC	TGT	GAA	TGG	TCT	CAA	CTA	ACC	CTT	TCA	GGT	CTA	1437
Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu	Ser	Gly	Leu	
			390				395					400				
AAT	GGA	GCC	CAG	ATG	GAG	AAA	ATA	CCC	CTA	TTG	CAT	ATT	TCT	TCA	TGT	1485
Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile	Ser	Ser	Cys	
	405					410					415					
GAC	CAA	AAT	ATT	TCA	GAA	AAA	GAC	CTA	TTA	GAC	ACA	GAG	AAC	AAA	AGA	1533
Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu	Asn	Lys	Arg	
420					425					430					435	
AAG	AAA	GAT	TTT	CTT	ACT	TCA	GAG	AAT	TCT	TTG	CCA	CGT	ATT	TCT	AGC	1581
Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg	Ile	Ser	Ser	
				440					445					450		
CTA	CCA	AAA	TCA	GAG	AAG	CCA	TTA	AAT	GAG	GAA	ACA	GTG	GTA	AAT	AAG	1629
Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val	Val	Asn	Lys	
			455					460					465			
AGA	GAT	GAA	GAG	CAG	CAT	CTT	GAA	TCT	CAT	ACA	GAC	TGC	ATT	CTT	GCA	1677
Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys	Ile	Leu	Ala	

470 475 480

GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG 1725
Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln
485 490 495

GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT 1773
Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr
500 505 510 515

TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA 1821
Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys
520 525 530

GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA 1869
Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser
535 540 545

CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG 1917
Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp
550 555 560

CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA 1965
Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu
565 570 575

ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT 2013
Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His
580 585 590 595

GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA 2061
Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser
600 605 610

GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA 2109
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala
615 620 625

CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG 2157
Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val
630 635 640

AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA 2205
Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu
645 650 655

ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA 2253
Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr
660 665 670 675

TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA 2301
Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala
680 685 690

AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT 2349
Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp
695 700 705

TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC 2397
 Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser
 710 715 720

AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC 2445
 Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Cys His
 725 730 735

CCA GTA CAA CAC TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC 2493
 Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser
 740 745 750 755

CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA 2541
 Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu
 760 765 770

ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA 2589
 Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg
 775 780 785

GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT 2637
 Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr
 790 795 800

GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA 2685
 Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln
 805 810 815

GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA 2733
 Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro
 820 825 830 835

CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC 2781
 Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe
 840 845 850

AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT 2829
 Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr
 855 860 865

ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC 2877
 Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe
 870 875 880

TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT 2925
 Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn
 885 890 895

AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT 2973
 Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr
 900 905 910 915

TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA 3021
 Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly
 920 925 930

GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG 3069
 Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu
 935 940 945

GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA 3117
 Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile
 950 955 960

AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA 3165
 Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile
 965 970 975

GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG GAC AAA TGG GCA GGA 3213
 Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys Trp Ala Gly
 980 985 990 995

CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA 3261
 Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr
 1000 1005 1010

GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC 3309
 Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser
 1015 1020 1025

AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT 3357
 Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala
 1030 1035 1040

TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG 3405
 Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu
 1045 1050 1055

AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT 3453
 Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser
 1060 1065 1070 1075

GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA 3501
 Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu
 1080 1085 1090

TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA 3549
 Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln
 1095 1100 1105

AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT 3597
 Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser
 1110 1115 1120

CAG TTT GAA TTT ACT CAG TTT AGA AAG CCA AGC TAC ATA TTG CAG AAG 3645
 Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys
 1125 1130 1135

AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT 3693
 Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr
 1140 1145 1150 1155

TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA 3741

Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro	
1160 1165 1170	
TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA	3789
Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu	
1175 1180 1185	
ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT	3837
Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser	
1190 1195 1200	
GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT	3885
Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe	
1205 1210 1215	
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA	3933
Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln	
1220 1225 1230 1235	
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT	3981
Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr	
1240 1245 1250	
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT	4029
Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp	
1255 1260 1265	
TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA	4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val	
1270 1275 1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA	4125
Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Asn Asn Ile Glu	
1285 1290 1295	
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA	4173
Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg	
1300 1305 1310 1315	
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT	4221
Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser	
1320 1325 1330	
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT	4269
His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val	
1335 1340 1345	
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC	4317
Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn	
1350 1355 1360	
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG	4365
Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln	
1365 1370 1375	
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT	4413
Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala	

1380	1385	1390	1395	
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT				4461
Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala	1400	1405	1410	
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT				4509
Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe	1415	1420	1425	
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT				4557
Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe	1430	1435	1440	
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC				4605
Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn	1445	1450	1455	
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG				4653
Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met	1460	1465	1470	1475
GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG				4701
Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu	1480	1485	1490	
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG				4749
Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln	1495	1500	1505	
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT				4797
Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly	1510	1515	1520	
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG				4845
Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu	1525	1530	1535	
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA				4893
Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu	1540	1545	1550	1555
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG				4941
Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu	1560	1565	1570	
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT				4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala	1575	1580	1585	
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC				5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn	1590	1595	1600	
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT				5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn	1605	1610	1615	

TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG 5133
 Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu
 1620 1625 1630 1635

AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT 5181
 Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro
 1640 1645 1650

GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA 5229
 Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser
 1655 1660 1665

GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG 5277
 Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln
 1670 1675 1680

ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT 5325
 Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp
 1685 1690 1695

GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG 5373
 Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu
 1700 1705 1710 1715

TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT 5421
 Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His
 1720 1725 1730

CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC 5469
 Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn
 1735 1740 1745

AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC 5517
 Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu
 1750 1755 1760

TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT 5565
 Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val
 1765 1770 1775

GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA 5613
 Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys
 1780 1785 1790 1795

GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG 5661
 Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu
 1800 1805 1810

GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT 5709
 Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile
 1815 1820 1825

AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA 5757
 Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala
 1830 1835 1840

TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT 5805
 Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile
 1845 1850 1855

AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG 5853
 Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys
 1860 1865 1870 1875

GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA 5901
 Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala
 1880 1885 1890

GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT 5949
 Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser
 1895 1900 1905

CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC 5997
 Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp
 1910 1915 1920

ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG 6045
 Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu
 1925 1930 1935

GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA 6093
 Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser
 1940 1945 1950 1955

GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT 6141
 Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser
 1960 1965 1970

GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG 6189
 Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln
 1975 1980 1985

GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA 6237
 Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile
 1990 1995 2000

GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC 6285
 Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn
 2005 2010 2015

GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT 6333
 Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr
 2020 2025 2030 2035

CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT 6381
 Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn
 2040 2045 2050

TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC 6429
 Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser
 2055 2060 2065

ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT 6477

Ile	Leu	Glu	Ser	Ser	Leu	His	Lys	Val	Lys	Gly	Val	Leu	Glu	Glu	Phe	
2070							2075					2080				
GAT	TTA	ATC	AGA	ACT	GAG	CAT	AGT	CTT	CAC	TAT	TCA	CCT	ACG	TCT	AGA	6525
Asp	Leu	Ile	Arg	Thr	Glu	His	Ser	Leu	His	Tyr	Ser	Pro	Thr	Ser	Arg	
2085						2090					2095					
CAA	AAT	GTA	TCA	AAA	ATA	CTT	CCT	CGT	GTT	GAT	AAG	AGA	AAC	CCA	GAG	6573
Gln	Asn	Val	Ser	Lys	Ile	Leu	Pro	Arg	Val	Asp	Lys	Arg	Asn	Pro	Glu	
2100				2105					2110					2115		
CAC	TGT	GTA	AAC	TCA	GAA	ATG	GAA	AAA	ACC	TGC	AGT	AAA	GAA	TTT	AAA	6621
His	Cys	Val	Asn	Ser	Glu	Met	Glu	Lys	Thr	Cys	Ser	Lys	Glu	Phe	Lys	
			2120					2125					2130			
TTA	TCA	AAT	AAC	TTA	AAT	GTT	GAA	GGT	GGT	TCT	TCA	GAA	AAT	AAT	CAC	6669
Leu	Ser	Asn	Asn	Leu	Asn	Val	Glu	Gly	Gly	Ser	Ser	Glu	Asn	Asn	His	
		2135				2140						2145				
TCT	ATT	AAA	GTT	TCT	CCA	TAT	CTC	TCT	CAA	TTT	CAA	CAA	GAC	AAA	CAA	6717
Ser	Ile	Lys	Val	Ser	Pro	Tyr	Leu	Ser	Gln	Phe	Gln	Gln	Asp	Lys	Gln	
	2150					2155				2160						
CAG	TTG	GTA	TTA	GGA	ACC	AAA	GTC	TCA	CTT	GTT	GAG	AAC	ATT	CAT	GTT	6765
Gln	Leu	Val	Leu	Gly	Thr	Lys	Val	Ser	Leu	Val	Glu	Asn	Ile	His	Val	
2165					2170					2175						
TTG	GGA	AAA	GAA	CAG	GCT	TCA	CCT	AAA	AAC	GTA	AAA	ATG	GAA	ATT	GGT	6813
Leu	Gly	Lys	Glu	Gln	Ala	Ser	Pro	Lys	Asn	Val	Lys	Met	Glu	Ile	Gly	
2180				2185				2190				2195				
AAA	ACT	GAA	ACT	TTT	TCT	GAT	GTT	CCT	GTG	AAA	ACA	AAT	ATA	GAA	GTT	6861
Lys	Thr	Glu	Thr	Phe	Ser	Asp	Val	Pro	Val	Lys	Thr	Asn	Ile	Glu	Val	
			2200				2205					2210				
TGT	TCT	ACT	TAC	TCC	AAA	GAT	TCA	GAA	AAC	TAC	TTT	GAA	ACA	GAA	GCA	6909
Cys	Ser	Thr	Tyr	Ser	Lys	Asp	Ser	Glu	Asn	Tyr	Phe	Glu	Thr	Glu	Ala	
		2215				2220						2225				
GTA	GAA	ATT	GCT	AAA	GCT	TTT	ATG	GAA	GAT	GAT	GAA	CTG	ACA	GAT	TCT	6957
Val	Glu	Ile	Ala	Lys	Ala	Phe	Met	Glu	Asp	Asp	Glu	Leu	Thr	Asp	Ser	
	2230				2235						2240					
AAA	CTG	CCA	AGT	CAT	GCC	ACA	CAT	TCT	CTT	TTT	ACA	TGT	CCC	GAA	AAT	7005
Lys	Leu	Pro	Ser	His	Ala	Thr	His	Ser	Leu	Phe	Thr	Cys	Pro	Glu	Asn	
2245				2250						2255						
GAG	GAA	ATG	GTT	TTG	TCA	AAT	TCA	AGA	ATT	GGA	AAA	AGA	AGA	GGA	GAG	7053
Glu	Glu	Met	Val	Leu	Ser	Asn	Ser	Arg	Ile	Gly	Lys	Arg	Arg	Gly	Glu	
2260				2265				2270				2275				
CCC	CTT	ATC	TTA	GTG	GGA	GAA	CCC	TCA	ATC	AAA	AGA	AAC	TTA	TTA	AAT	7101
Pro	Leu	Ile	Leu	Val	Gly	Glu	Pro	Ser	Ile	Lys	Arg	Asn	Leu	Leu	Asn	
			2280				2285					2290				
GAA	TTT	GAC	AGG	ATA	ATA	GAA	AAT	CAA	GAA	AAA	TCC	TTA	AAG	GCT	TCA	7149
Glu	Phe	Asp	Arg	Ile	Ile	Glu	Asn	Gln	Glu	Lys	Ser	Leu	Lys	Ala	Ser	

2295 2300 2305

AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT 7197
 Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His
 2310 2315 2320

CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG 7245
 His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys
 2325 2330 2335

GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA 7293
 Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu
 2340 2345 2350 2355

TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT 7341
 Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser
 2360 2365 2370

TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT 7389
 Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala
 2375 2380 2385

ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC 7437
 Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr
 2390 2395 2400

AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCG CAT TTT CAC AGA GTT 7485
 Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val
 2405 2410 2415

GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA 7533
 Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln
 2420 2425 2430 2435

AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC 7581
 Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp
 2440 2445 2450

AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT 7629
 Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala
 2455 2460 2465

GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT 7677
 Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser
 2470 2475 2480

CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA 7725
 Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln
 2485 2490 2495

AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA 7773
 Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr
 2500 2505 2510 2515

TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT 7821
 Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val
 2520 2525 2530

CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA 7869
 Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys
 2535 2540 2545

CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC 7917
 His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His
 2550 2555 2560

ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA 7965
 Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile
 2565 2570 2575

CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT 8013
 Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala
 2580 2585 2590 2595

GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT 8061
 Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp
 2600 2605 2610

CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC 8109
 Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile
 2615 2620 2625

ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT 8157
 Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala
 2630 2635 2640

AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA 8205
 Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg
 2645 2650 2655

TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA 8253
 Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile
 2660 2665 2670 2675

ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT 8301
 Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser
 2680 2685 2690

GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA 8349
 Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys
 2695 2700 2705

ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT 8397
 Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp
 2710 2715 2720

GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC 8445
 Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val
 2725 2730 2735

TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA 8493
 Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly
 2740 2745 2750 2755

GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA 8541
 Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro
 2760 2765 2770

GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC 8589
 Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg
 2775 2780 2785

TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG 8637
 Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu
 2790 2795 2800

CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT 8685
 Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp
 2805 2810 2815

GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA 8733
 Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser
 2820 2825 2830 2835

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA 8781
 Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala
 2840 2845 2850

GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT 8829
 Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr
 2855 2860 2865

AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA 8877
 Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro
 2870 2875 2880

TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA 8925
 Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln
 2885 2890 2895

GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT 8973
 Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala
 2900 2905 2910 2915

TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT 9021
 Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn
 2920 2925 2930

CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA 9069
 His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu
 2935 2940 2945

ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA 9117
 Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser
 2950 2955 2960

AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA 9165
 Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys
 2965 2970 2975

AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT 9213

Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp
 2980 2985 2990 2995

TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT 9261
 Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu
 3000 3005 3010

GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA 9309
 Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu
 3015 3020 3025

GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA 9357
 Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu
 3030 3035 3040

ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA 9405
 Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys
 3045 3050 3055

TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA 9453
 Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile
 3060 3065 3070 3075

GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC 9501
 Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val
 3080 3085 3090

TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA 9549
 Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile
 3095 3100 3105

GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC 9597
 Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser
 3110 3115 3120

AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT 9645
 Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe
 3125 3130 3135

GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT 9693
 Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe
 3140 3145 3150 3155

CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA 9741
 Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile
 3160 3165 3170

CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT 9789
 Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn
 3175 3180 3185

GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC 9837
 Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr
 3190 3195 3200

ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT 9885
 Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser

3205 3210 3215

CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC 9933
 Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala
 3220 3225 3230 3235

AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG 9981
 Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys
 3240 3245 3250

TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG 10029
 Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys
 3255 3260 3265

AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT 10077
 Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Val
 3270 3275 3280

AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG 10125
 Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln
 3285 3290 3295

CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA 10173
 Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys
 3300 3305 3310 3315

GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT 10221
 Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile
 3320 3325 3330

TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA 10269
 Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile
 3335 3340 3345

AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA 10317
 Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile
 3350 3355 3360

TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT 10365
 Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr
 3365 3370 3375

CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413
 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu
 3380 3385 3390 3395

AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461
 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr
 3400 3405 3410

ATT ACA ACT AAA AAA TAT ATC TAA 10485
 Ile Thr Thr Lys Lys Tyr Ile
 3415

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys
1 5 10 15
Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
20 25 30
Glu Glu Leu Ser Ser Glu Ala Pro Tyr Asn Ser Glu Pro Ala Glu
35 40 45
Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
50 55 60
Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
65 70 75 80
Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
85 90 95
Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
100 105 110
Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
115 120 125
Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
130 135 140
Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
145 150 155 160
Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
165 170 175
Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
180 185 190
Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
195 200 205
Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
210 215 220
Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
225 230 235 240
Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
245 250 255
Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
260 265 270
Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
275 280 285
His Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
290 295 300
Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
305 310 315 320
Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
325 330 335
Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
340 345 350
Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
355 360 365

Asn Val Ala Asn Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
 370 375 380
 Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
 385 390 395 400
 Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
 405 410 415
 Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
 420 425 430
 Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
 435 440 445
 Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
 450 455 460
 Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
 465 470 475 480
 Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
 485 490 495
 Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
 500 505 510
 Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
 515 520 525
 Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
 530 535 540
 Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
 545 550 555 560
 Gly Ser Trp Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
 565 570 575
 Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
 580 585 590
 Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
 595 600 605
 Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
 610 615 620
 Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
 625 630 635 640
 Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
 645 650 655
 Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
 660 665 670
 Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
 675 680 685
 Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
 690 695 700
 Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
 705 710 715 720
 Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
 725 730 735
 Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
 740 745 750
 Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
 755 760 765
 Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
 770 775 780
 Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
 785 790 795 800
 Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
 805 810 815
 Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu

820 825 830
 Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
 835 840 845
 Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
 850 855 860
 Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
 865 870 875 880
 Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
 885 890 895
 Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
 900 905 910
 Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
 915 920 925
 Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
 930 935 940
 Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
 945 950 955 960
 Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
 965 970 975
 Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys
 980 985 990
 Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
 995 1000 1005
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
 1010 1015 1020
 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
 1025 1030 1035 104
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
 1045 1050 1055
 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
 1060 1065 1070
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
 1075 1080 1085
 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
 1090 1095 1100
 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
 1105 1110 1115 112
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
 1125 1130 1135
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
 1140 1145 1150
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
 1155 1160 1165
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
 1170 1175 1180
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
 1185 1190 1195 120
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
 1205 1210 1215
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
 1220 1225 1230
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
 1235 1240 1245
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys
 1250 1255 1260
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
 1265 1270 1275 128

Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
 1285 1290 1295
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
 1300 1305 1310
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
 1315 1320 1325
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 136
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 144
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
 1460 1465 1470
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
 1475 1480 1485
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
 1490 1495 1500
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
 1505 1510 1515 152
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
 1525 1530 1535
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
 1540 1545 1550
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
 1555 1560 1565
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
 1570 1575 1580
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
 1585 1590 1595 160
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
 1605 1610 1615
 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
 1620 1625 1630
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
 1635 1640 1645
 Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
 1650 1655 1660
 Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
 1665 1670 1675 168
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
 1685 1690 1695
 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
 1700 1705 1710
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
 1715 1720 1725
 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser

1730 1735 1740
 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
 1745 1750 1755 176
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
 1765 1770 1775
 Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
 1780 1785 1790
 Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
 1795 1800 1805
 Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn
 1810 1815 1820
 Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
 1825 1830 1835 184
 Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
 1845 1850 1855
 Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
 1860 1865 1870
 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
 1875 1880 1885
 Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
 1890 1895 1900
 His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
 1905 1910 1915 192
 Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
 1925 1930 1935
 Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
 1940 1945 1950
 Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
 1955 1960 1965
 Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
 1970 1975 1980
 Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
 1985 1990 1995 200
 Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
 2005 2010 2015
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
 2020 2025 2030
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
 2035 2040 2045
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
 2050 2055 2060
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
 2065 2070 2075 208
 Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
 2085 2090 2095
 Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
 2100 2105 2110
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
 2115 2120 2125
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
 2130 2135 2140
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
 2145 2150 2155 216
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
 2165 2170 2175
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
 2180 2185 2190

Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
 2195 2200 2205
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
 2210 2215 2220
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
 2225 2230 2235 224
 Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
 2245 2250 2255
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
 2260 2265 2270
 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
 2275 2280 2285
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
 2290 2295 2300
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
 2305 2310 2315 232
 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
 2325 2330 2335
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
 2340 2345 2350
 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
 2355 2360 2365
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
 2370 2375 2380
 Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
 2385 2390 2395 240
 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
 2405 2410 2415
 His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
 2420 2425 2430
 Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
 2435 2440 2445
 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
 2450 2455 2460
 Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu
 2465 2470 2475 248
 Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
 2485 2490 2495
 Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
 2500 2505 2510
 Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly
 2515 2520 2525
 Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly
 2530 2535 2540
 Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe
 2545 2550 2555 256
 Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly
 2565 2570 2575
 Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp
 2580 2585 2590
 Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro
 2595 2600 2605
 Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr
 2610 2615 2620
 Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys
 2625 2630 2635 264
 Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu

2645 2650 2655
 Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile
 2660 2665 2670
 Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
 2675 2680 2685
 Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
 2690 2695 2700
 Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
 2705 2710 2715 272
 Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
 2725 2730 2735
 Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile
 2740 2745 2750
 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
 2755 2760 2765
 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
 2770 2775 2780
 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
 2785 2790 2795 280
 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
 2805 2810 2815
 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
 2820 2825 2830
 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu
 2835 2840 2845
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
 2850 2855 2860
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
 2865 2870 2875 288
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
 2885 2890 2895
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
 2900 2905 2910
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
 2915 2920 2925
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
 2930 2935 2940
 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
 2945 2950 2955 296
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
 2965 2970 2975
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
 2980 2985 2990
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
 2995 3000 3005
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
 3010 3015 3020
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
 3025 3030 3035 304
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
 3045 3050 3055
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
 3060 3065 3070
 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
 3075 3080 3085
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
 3090 3095 3100

Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
 3105 3110 3115 312
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
 3125 3130 3135
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
 3140 3145 3150
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
 3155 3160 3165
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
 3170 3175 3180
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
 3185 3190 3195 320
 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
 3205 3210 3215
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
 3220 3225 3230
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
 3235 3240 3245
 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
 3250 3255 3260
 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
 3265 3270 3275 328
 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
 3285 3290 3295
 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
 3300 3305 3310
 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
 3315 3320 3325
 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
 3330 3335 3340
 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
 3345 3350 3355 336
 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser
 3365 3370 3375
 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys
 3380 3385 3390
 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
 3395 3400 3405
 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile
 3410 3415

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI4)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC 60
TCTGCTGCGC CTCGGGTGTC TTTTGC GGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG 120
ACAGATTGT GACCGGCGCG GTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT 180
CTGGAGCGGA CTTATTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT 237
Met Pro Ile
1

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC 285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
5 10 15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT 333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu
20 25 30 35

TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA 381
Ser Ser Glu Ala Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu
40 45 50

CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG 429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg
55 60 65

AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG 477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu
70 75 80

CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT 525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp
85 90 95

AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA 573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys
100 105 110 115

AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC 621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser
120 125 130

TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA 669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln
135 140 145

TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT 717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser
150 155 160

TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT 765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His
165 170 175

ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA 813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser
180 185 190 195

AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC 861

Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val	Leu	Ile	Val	
				200					205					210		
AGA	AAT	GAA	GAA	GCA	TCT	GAA	ACT	GTA	TTT	CCT	CAT	GAT	ACT	ACT	GCT	909
Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp	Thr	Thr	Ala	
			215					220					225			
AAT	GTG	AAA	AGC	TAT	TTT	TCC	AAT	CAT	GAT	GAA	AGT	CTG	AAG	AAA	AAT	957
Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu	Lys	Lys	Asn	
		230					235					240				
GAT	AGA	TTT	ATC	GCT	TCT	GTG	ACA	GAC	AGT	GAA	AAC	ACA	AAT	CAA	AGA	1005
Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr	Asn	Gln	Arg	
	245					250					255					
GAA	GCT	GCA	AGT	CAT	GGA	TTT	GGA	AAA	ACA	TCA	GGG	AAT	TCA	TTT	AAA	1053
Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn	Ser	Phe	Lys	
260					265				270						275	
GTA	AAT	AGC	TGC	AAA	GAC	CAC	ATT	GGA	AAG	TCA	ATG	CCA	AAT	GTC	CTA	1101
Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro	Asn	Val	Leu	
			280					285						290		
GAA	GAT	GAA	GTA	TAT	GAA	ACA	GTT	GTA	GAT	ACC	TCT	GAA	GAA	GAT	AGT	1149
Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu	Glu	Asp	Ser	
			295				300						305			
TTT	TCA	TTA	TGT	TTT	TCT	AAA	TGT	AGA	ACA	AAA	AAT	CTA	CAA	AAA	GTA	1197
Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu	Gln	Lys	Val	
		310					315					320				
AGA	ACT	AGC	AAG	ACT	AGG	AAA	AAA	ATT	TTC	CAT	GAA	GCA	AAC	GCT	GAT	1245
Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala	Asn	Ala	Asp	
	325					330					335					
GAA	TGT	GAA	AAA	TCT	AAA	AAC	CAA	GTG	AAA	GAA	AAA	TAC	TCA	TTT	GTA	1293
Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr	Ser	Phe	Val	
340					345				350						355	
TCT	GAA	GTG	GAA	CCA	AAT	GAT	ACT	GAT	CCA	TTA	GAT	TCA	AAT	GTA	GCA	1341
Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser	Asn	Val	Ala	
			360					365						370		
CAT	CAG	AAG	CCC	TTT	GAG	AGT	GGA	AGT	GAC	AAA	ATC	TCC	AAG	GAA	GTT	1389
His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser	Lys	Glu	Val	
			375					380					385			
GTA	CCG	TCT	TTG	GCC	TGT	GAA	TGG	TCT	CAA	CTA	ACC	CTT	TCA	GGT	CTA	1437
Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu	Ser	Gly	Leu	
		390					395					400				
AAT	GGA	GCC	CAG	ATG	GAG	AAA	ATA	CCC	CTA	TTG	CAT	ATT	TCT	TCA	TGT	1485
Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile	Ser	Ser	Cys	
	405					410					415					
GAC	CAA	AAT	ATT	TCA	GAA	AAA	GAC	CTA	TTA	GAC	ACA	GAG	AAC	AAA	AGA	1533
Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu	Asn	Lys	Arg	

420	425	430	435	
AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC				1581
Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser	440	445	450	
CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG				1629
Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys	455	460	465	
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA				1677
Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala	470	475	480	
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG				1725
Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln	485	490	495	
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT				1773
Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr	500	505	510	515
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA				1821
Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys	520	525	530	
GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA				1869
Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser	535	540	545	
CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG				1917
Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp	550	555	560	
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA				1965
Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu	565	570	575	
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT				2013
Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His	580	585	590	595
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA				2061
Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser	600	605	610	
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA				2109
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala	615	620	625	
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG				2157
Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val	630	635	640	
AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA				2205
Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu	645	650	655	

ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA 2253
 Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr
 660 665 670 675

TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA 2301
 Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala
 680 685 690

AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT 2349
 Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp
 695 700 705

TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC 2397
 Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser
 710 715 720

AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC 2445
 Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His
 725 730 735

CCA GTA CAA CAT TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC 2493
 Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser
 740 745 750 755

CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA 2541
 Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu
 760 765 770

ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA 2589
 Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg
 775 780 785

GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT 2637
 Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr
 790 795 800

GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA 2685
 Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln
 805 810 815

GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA 2733
 Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro
 820 825 830 835

CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC 2781
 Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe
 840 845 850

AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT 2829
 Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr
 855 860 865

ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC 2877
 Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe
 870 875 880

TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn 885 890 895	2925
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr 900 905 910 915	2973
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly 920 925 930	3021
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu 935 940 945	3069
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile 950 955 960	3117
AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile 965 970 975	3165
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly 980 985 990 995	3213
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr 1000 1005 1010	3261
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser 1015 1020 1025	3309
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala 1030 1035 1040	3357
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu 1045 1050 1055	3405
AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser 1060 1065 1070 1075	3453
GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu 1080 1085 1090	3501
TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln 1095 1100 1105	3549
AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT	3597

Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser
 1110 1115 1120

CAG TTT GAA TTT ACT CAG TTT AGA AAG CCA AGC TAC ATA TTG CAG AAG 3645
 Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys
 1125 1130 1135

AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT 3693
 Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr
 1140 1145 1150 1155

TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA 3741
 Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro
 1160 1165 1170

TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA 3789
 Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu
 1175 1180 1185

ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT 3837
 Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser
 1190 1195 1200

GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT 3885
 Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe
 1205 1210 1215

TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA 3933
 Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln
 1220 1225 1230 1235

AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT 3981
 Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr
 1240 1245 1250

TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT 4029
 Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp
 1255 1260 1265

TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA 4077
 Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val
 1270 1275 1280

AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA 4125
 Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu
 1285 1290 1295

ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA 4173
 Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg
 1300 1305 1310 1315

AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT 4221
 Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser
 1320 1325 1330

CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT 4269
 His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val

1335	1340	1345	
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn 1350 1355 1360			4317
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln 1365 1370 1375			4365
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala 1380 1385 1390 1395			4413
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala 1400 1405 1410			4461
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe 1415 1420 1425			4509
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe 1430 1435 1440			4557
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn 1445 1450 1455			4605
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met 1460 1465 1470 1475			4653
GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu 1480 1485 1490			4701
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln 1495 1500 1505			4749
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly 1510 1515 1520			4797
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu 1525 1530 1535			4845
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu 1540 1545 1550 1555			4893
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu 1560 1565 1570			4941

GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT	4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala	
1575 1580 1585	
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC	5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn	
1590 1595 1600	
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT	5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn	
1605 1610 1615	
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG	5133
Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu	
1620 1625 1630 1635	
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT	5181
Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro	
1640 1645 1650	
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA	5229
Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser	
1655 1660 1665	
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG	5277
Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln	
1670 1675 1680	
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT	5325
Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp	
1685 1690 1695	
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG	5373
Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu	
1700 1705 1710 1715	
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT	5421
Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His	
1720 1725 1730	
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC	5469
Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn	
1735 1740 1745	
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC	5517
Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu	
1750 1755 1760	
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT	5565
Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val	
1765 1770 1775	
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA	5613
Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys	
1780 1785 1790 1795	

GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu 1800 1805 1810	5661
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile 1815 1820 1825	5709
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala 1830 1835 1840	5757
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile 1845 1850 1855	5805
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys 1860 1865 1870 1875	5853
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala 1880 1885 1890	5901
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser 1895 1900 1905	5949
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp 1910 1915 1920	5997
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu 1925 1930 1935	6045
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser 1940 1945 1950 1955	6093
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser 1960 1965 1970	6141
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln 1975 1980 1985	6189
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile 1990 1995 2000	6237
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn 2005 2010 2015	6285
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT	6333

Glu 2020	His	Ser	Asp	Gln	Leu	Thr	Arg	Glu	Asn	Thr	Ala	Ile	Arg	Thr		
				2025				2030				2035				
CCA Pro	GAA Glu	CAT His	TTA Leu	ATA Ile	TCC Ser	CAA Gln	AAA Lys	GGC Gly	TTT Phe	TCA Ser	TAT Tyr	AAT Asn	GTG Val	GTA Val	AAT Asn	6381
				2040				2045				2050				
TCA Ser	TCT Ser	GCT Ala	TTC Phe	TCT Ser	GGA Gly	TTT Phe	AGT Ser	ACA Thr	GCA Ala	AGT Ser	GGA Gly	AAG Lys	CAA Gln	GTT Val	TCC Ser	6429
				2055				2060				2065				
ATT Ile	TTA Leu	GAA Glu	AGT Ser	TCC Ser	TTA Leu	CAC His	AAA Lys	GTT Val	AAG Lys	GGA Gly	GTG Val	TTA Leu	GAG Glu	GAA Glu	TTT Phe	6477
				2070				2075				2080				
GAT Asp	TTA Leu	ATC Ile	AGA Arg	ACT Thr	GAG Glu	CAT His	AGT Ser	CTT Leu	CAC His	TAT Tyr	TCA Ser	CCT Pro	ACG Thr	TCT Ser	AGA Arg	6525
				2085				2090				2095				
CAA Gln	AAT Asn	GTA Val	TCA Ser	AAA Lys	ATA Ile	CTT Leu	CCT Pro	CGT Arg	GTT Val	GAT Asp	AAG Lys	AGA Arg	AAC Asn	CCA Pro	GAG Glu	6573
2100				2105				2110				2115				
CAC His	TGT Cys	GTA Val	AAC Asn	TCA Ser	GAA Glu	ATG Met	GAA Glu	AAA Lys	ACC Thr	TGC Cys	AGT Ser	AAA Lys	GAA Glu	TTT Phe	AAA Lys	6621
				2120				2125				2130				
TTA Leu	TCA Ser	AAT Asn	AAC Asn	TTA Leu	AAT Asn	GTT Val	GAA Glu	GGT Gly	GGT Gly	TCT Ser	TCA Ser	GAA Glu	AAT Asn	AAT Asn	CAC His	6669
				2135				2140				2145				
TCT Ser	ATT Ile	AAA Lys	GTT Val	TCT Ser	CCA Pro	TAT Tyr	CTC Leu	TCT Ser	CAA Gln	TTT Phe	CAA Gln	CAA Gln	GAC Asp	AAA Lys	CAA Gln	6717
				2150				2155				2160				
CAG Gln	TTG Leu	GTA Val	TTA Leu	GGA Gly	ACC Thr	AAA Lys	GTC Val	TCA Ser	CTT Leu	GTT Val	GAG Glu	AAC Asn	ATT Ile	CAT His	GTT Val	6765
				2165				2170				2175				
TTG Leu	GGA Gly	AAA Lys	GAA Glu	CAG Gln	GCT Ala	TCA Ser	CCT Pro	AAA Lys	AAC Asn	GTA Val	AAA Lys	ATG Met	GAA Glu	ATT Ile	GGT Gly	6813
2180				2185				2190				2195				
AAA Lys	ACT Thr	GAA Glu	ACT Thr	TTT Phe	TCT Ser	GAT Asp	GTT Val	CCT Pro	GTG Val	AAA Lys	ACA Thr	AAT Asn	ATA Ile	GAA Glu	GTT Val	6861
				2200				2205				2210				
TGT Cys	TCT Ser	ACT Thr	TAC Tyr	TCC Ser	AAA Lys	GAT Asp	TCA Ser	GAA Glu	AAC Asn	TAC Tyr	TTT Phe	GAA Glu	ACA Thr	GAA Glu	GCA Ala	6909
				2215				2220				2225				
GTA Val	GAA Glu	ATT Ile	GCT Ala	AAA Lys	GCT Ala	TTT Phe	ATG Met	GAA Glu	GAT Asp	GAT Asp	GAA Glu	CTG Leu	ACA Thr	GAT Asp	TCT Ser	6957
				2230				2235				2240				
AAA Lys	CTG Leu	CCA Pro	AGT Ser	CAT His	GCC Ala	ACA Thr	CAT His	TCT Ser	CTT Leu	TTT Phe	ACA Thr	TGT Cys	CCC Pro	GAA Glu	AAT Asn	7005

2245	2250	2255	
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG			7053
Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu			
2260	2265	2270	2275
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT			7101
Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn			
2280	2285	2290	
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA			7149
Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser			
2295	2300	2305	
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT			7197
Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His			
2310	2315	2320	
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG			7245
His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys			
2325	2330	2335	
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA			7293
Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu			
2340	2345	2350	2355
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT			7341
Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser			
2360	2365	2370	
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT			7389
Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala			
2375	2380	2385	
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC			7437
Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr			
2390	2395	2400	
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCG CAT TTT CAC AGA GTT			7485
Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val			
2405	2410	2415	
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA			7533
Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln			
2420	2425	2430	2435
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC			7581
Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp			
2440	2445	2450	
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT			7629
Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala			
2455	2460	2465	
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT			7677
Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser			
2470	2475	2480	

CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln 2485 2490 2495	7725
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr 2500 2505 2510 2515	7773
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val 2520 2525 2530	7821
CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys 2535 2540 2545	7869
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His 2550 2555 2560	7917
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile 2565 2570 2575	7965
CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala 2580 2585 2590 2595	8013
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp 2600 2605 2610	8061
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile 2615 2620 2625	8109
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala 2630 2635 2640	8157
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg 2645 2650 2655	8205
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile 2660 2665 2670 2675	8253
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser 2680 2685 2690	8301
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys 2695 2700 2705	8349

ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp 2710 2715 2720	8397
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val 2725 2730 2735	8445
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly 2740 2745 2750 2755	8493
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro 2760 2765 2770	8541
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg 2775 2780 2785	8589
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu 2790 2795 2800	8637
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp 2805 2810 2815	8685
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser 2820 2825 2830 2835	8733
TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala 2840 2845 2850	8781
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr 2855 2860 2865	8829
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro 2870 2875 2880	8877
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln 2885 2890 2895	8925
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala 2900 2905 2910 2915	8973
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn 2920 2925 2930	9021
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA	9069

His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu	
2935 2940 2945	
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA	9117
Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser	
2950 2955 2960	
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA	9165
Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys	
2965 2970 2975	
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT	9213
Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp	
2980 2985 2990 2995	
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT	9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu	
3000 3005 3010	
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA	9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu	
3015 3020 3025	
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA	9357
Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu	
3030 3035 3040	
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA	9405
Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys	
3045 3050 3055	
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA	9453
Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile	
3060 3065 3070 3075	
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC	9501
Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val	
3080 3085 3090	
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA	9549
Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile	
3095 3100 3105	
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC	9597
Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser	
3110 3115 3120	
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT	9645
Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe	
3125 3130 3135	
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT	9693
Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe	
3140 3145 3150 3155	
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA	9741
Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile	

	3160	3165	3170	
	CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn 3175 3180 3185	9789		
	GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr 3190 3195 3200	9837		
	ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser 3205 3210 3215	9885		
a	CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala 3220 3225 3230 3235	9933		
	AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys 3240 3245 3250	9981		
	TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys 3255 3260 3265	10029		
	AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val 3270 3275 3280	10077		
	AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln 3285 3290 3295	10125		
	CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys 3300 3305 3310 3315	10173		
	GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile 3320 3325 3330	10221		
	TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile 3335 3340 3345	10269		
	AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile 3350 3355 3360	10317		
	TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr 3365 3370 3375	10365		
	CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu 3380 3385 3390 3395	10413		

AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461
 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr
 3400 3405 3410

ATT ACA ACT AAA AAA TAT ATC TAA
 Ile Thr Thr Lys Lys Tyr Ile 10485
 3415

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3418 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Pro	Ile	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys	1	5	10	15
Thr	Arg	Cys	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe	20	25	30	
Glu	Glu	Leu	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu	35	40	45	
Glu	Ser	Glu	His	Lys	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr		50	55	60	
Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile	65	70	75	80
Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys	85	90	95	
Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser	100	105	110	
Arg	His	Lys	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp	115	120	125	
Asp	Val	Ser	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val	130	135	140	
Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val	145	150	155	160
Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr	165	170	175	
Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met	180	185	190	
Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val	195	200	205	
Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp	210	215	220	
Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu	225	230	235	240
Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr	245	250	255	
Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn	260	265	270	

Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
 275 280 285
 Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
 290 295 300
 Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
 305 310 315 320
 Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
 325 330 335
 Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
 340 345 350
 Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
 355 360 365
 Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
 370 375 380
 Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
 385 390 395 400
 Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
 405 410 415
 Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
 420 425 430
 Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
 435 440 445
 Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
 450 455 460
 Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
 465 470 475 480
 Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
 485 490 495
 Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
 500 505 510
 Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
 515 520 525
 Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
 530 535 540
 Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
 545 550 555 560
 Gly Ser Trp Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
 565 570 575
 Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
 580 585 590
 Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
 595 600 605
 Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
 610 615 620
 Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
 625 630 635 640
 Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
 645 650 655
 Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
 660 665 670
 Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
 675 680 685
 Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
 690 695 700
 Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
 705 710 715 720
 Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala

725 730 735
 Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
 740 745 750
 Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
 755 760 765
 Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
 770 775 780
 Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
 785 790 795 800
 Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
 805 810 815
 Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
 820 825 830
 Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
 835 840 845
 Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
 850 855 860
 Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
 865 870 875 880
 Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
 885 890 895
 Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
 900 905 910
 Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
 915 920 925
 Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
 930 935 940
 Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
 945 950 955 960
 Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
 965 970 975
 Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys
 980 985 990
 Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
 995 1000 1005
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
 1010 1015 1020
 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
 1025 1030 1035 104
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
 1045 1050 1055
 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
 1060 1065 1070
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
 1075 1080 1085
 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
 1090 1095 1100
 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
 1105 1110 1115 112
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
 1125 1130 1135
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
 1140 1145 1150
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
 1155 1160 1165
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
 1170 1175 1180

Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
 1185 1190 1195 120
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
 1205 1210 1215
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
 1220 1225 1230
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
 1235 1240 1245
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys
 1250 1255 1260
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
 1265 1270 1275 128
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
 1285 1290 1295
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
 1300 1305 1310
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
 1315 1320 1325
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 136
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 144
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
 1460 1465 1470
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
 1475 1480 1485
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
 1490 1495 1500
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
 1505 1510 1515 152
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Val Lys Ile Ala Lys
 1525 1530 1535
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
 1540 1545 1550
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
 1555 1560 1565
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
 1570 1575 1580
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
 1585 1590 1595 160
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
 1605 1610 1615
 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
 1620 1625 1630
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala

1635	1640	1645
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile		
1650	1655	1660
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser		
1665	1670	1675
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly		168
1685	1690	1695
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly		
1700	1705	1710
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp		
1715	1720	1725
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser		
1730	1735	1740
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser		
1745	1750	1755
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu		176
1765	1770	1775
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser		
1780	1785	1790
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile		
1795	1800	1805
Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn		
1810	1815	1820
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly		
1825	1830	1835
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His		184
1845	1850	1855
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys		
1860	1865	1870
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys		
1875	1880	1885
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu		
1890	1895	1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val		
1905	1910	1915
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met		192
1925	1930	1935
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu		
1940	1945	1950
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser		
1955	1960	1965
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys		
1970	1975	1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe		
1985	1990	1995
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe		200
2005	2010	2015
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala		
2020	2025	2030
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn		
2035	2040	2045
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys		
2050	2055	2060
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu		
2065	2070	2075
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro		
2085	2090	2095

Thr	Ser	Arg	Gln	Asn	Val	Ser	Lys	Ile	Leu	Pro	Arg	Val	Asp	Lys	Arg	2100	2105	2110
Asn	Pro	Glu	His	Cys	Val	Asn	Ser	Glu	Met	Glu	Lys	Thr	Cys	Ser	Lys	2115	2120	2125
Glu	Phe	Lys	Leu	Ser	Asn	Asn	Leu	Asn	Val	Glu	Gly	Gly	Ser	Ser	Glu	2130	2135	2140
Asn	Asn	His	Ser	Ile	Lys	Val	Ser	Pro	Tyr	Leu	Ser	Gln	Phe	Gln	Gln	2145	2150	2155
Asp	Lys	Gln	Gln	Leu	Val	Leu	Gly	Thr	Lys	Val	Ser	Leu	Val	Glu	Asn	2165	2170	2175
Ile	His	Val	Leu	Gly	Lys	Glu	Gln	Ala	Ser	Pro	Lys	Asn	Val	Lys	Met	2180	2185	2190
Glu	Ile	Gly	Lys	Thr	Glu	Thr	Phe	Ser	Asp	Val	Pro	Val	Lys	Thr	Asn	2195	2200	2205
Ile	Glu	Val	Cys	Ser	Thr	Tyr	Ser	Lys	Asp	Ser	Glu	Asn	Tyr	Phe	Glu	2210	2215	2220
Thr	Glu	Ala	Val	Glu	Ile	Ala	Lys	Ala	Phe	Met	Glu	Asp	Asp	Glu	Leu	2225	2230	2235
Thr	Asp	Ser	Lys	Leu	Pro	Ser	His	Ala	Thr	His	Ser	Leu	Phe	Thr	Cys	2245	2250	2255
Pro	Glu	Asn	Glu	Glu	Met	Val	Leu	Ser	Asn	Ser	Arg	Ile	Gly	Lys	Arg	2260	2265	2270
Arg	Gly	Glu	Pro	Leu	Ile	Leu	Val	Gly	Glu	Pro	Ser	Ile	Lys	Arg	Asn	2275	2280	2285
Leu	Leu	Asn	Glu	Phe	Asp	Arg	Ile	Ile	Glu	Asn	Gln	Glu	Lys	Ser	Leu	2290	2295	2300
Lys	Ala	Ser	Lys	Ser	Thr	Pro	Asp	Gly	Thr	Ile	Lys	Asp	Arg	Arg	Leu	2305	2310	2315
Phe	Met	His	His	Val	Ser	Leu	Glu	Pro	Ile	Thr	Cys	Val	Pro	Phe	Arg	2325	2330	2335
Thr	Thr	Lys	Glu	Arg	Gln	Glu	Ile	Gln	Asn	Pro	Asn	Phe	Thr	Ala	Pro	2340	2345	2350
Gly	Gln	Glu	Phe	Leu	Ser	Lys	Ser	His	Leu	Tyr	Glu	His	Leu	Thr	Leu	2355	2360	2365
Glu	Lys	Ser	Ser	Ser	Asn	Leu	Ala	Val	Ser	Gly	His	Pro	Phe	Tyr	Gln	2370	2375	2380
Val	Ser	Ala	Thr	Arg	Asn	Glu	Lys	Met	Arg	His	Leu	Ile	Thr	Thr	Gly	2385	2390	2395
Arg	Pro	Thr	Lys	Val	Phe	Val	Pro	Pro	Phe	Lys	Thr	Lys	Ser	His	Phe	2405	2410	2415
His	Arg	Val	Glu	Gln	Cys	Val	Arg	Asn	Ile	Asn	Leu	Glu	Glu	Asn	Arg	2420	2425	2430
Gln	Lys	Gln	Asn	Ile	Asp	Gly	His	Gly	Ser	Asp	Asp	Ser	Lys	Asn	Lys	2435	2440	2445
Ile	Asn	Asp	Asn	Glu	Ile	His	Gln	Phe	Asn	Lys	Asn	Asn	Ser	Asn	Gln	2450	2455	2460
Ala	Ala	Ala	Val	Thr	Phe	Thr	Lys	Cys	Glu	Glu	Glu	Pro	Leu	Asp	Leu	2465	2470	2475
Ile	Thr	Ser	Leu	Gln	Asn	Ala	Arg	Asp	Ile	Gln	Asp	Met	Arg	Ile	Lys	2485	2490	2495
Lys	Lys	Gln	Arg	Gln	Arg	Val	Phe	Pro	Gln	Pro	Gly	Ser	Leu	Tyr	Leu	2500	2505	2510
Ala	Lys	Thr	Ser	Thr	Leu	Pro	Arg	Ile	Ser	Leu	Lys	Ala	Ala	Val	Gly	2515	2520	2525
Gly	Gln	Val	Pro	Ser	Ala	Cys	Ser	His	Lys	Gln	Leu	Tyr	Thr	Tyr	Gly	2530	2535	2540
Val	Ser	Lys	His	Cys	Ile	Lys	Ile	Asn	Ser	Lys	Asn	Ala	Glu	Ser	Phe			

2545	2550	2555	256
Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly			
2565	2570	2575	
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp			
2580	2585	2590	
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro			
2595	2600	2605	
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr			
2610	2615	2620	
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys			
2625	2630	2635	264
Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu			
2645	2650	2655	
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile			
2660	2665	2670	
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu			
2675	2680	2685	
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser			
2690	2695	2700	
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu			
2705	2710	2715	272
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu			
2725	2730	2735	
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile			
2740	2745	2750	
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu			
2755	2760	2765	
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg			
2770	2775	2780	
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro			
2785	2790	2795	280
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly			
2805	2810	2815	
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu			
2820	2825	2830	
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu			
2835	2840	2845	
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala			
2850	2855	2860	
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr			
2865	2870	2875	288
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg			
2885	2890	2895	
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala			
2900	2905	2910	
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala			
2915	2920	2925	
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile			
2930	2935	2940	
Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln			
2945	2950	2955	296
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser			
2965	2970	2975	
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro			
2980	2985	2990	
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile			
2995	3000	3005	

Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
3010 3015 3020
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
3025 3030 3035 304
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
3045 3050 3055
Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
3060 3065 3070
Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
3075 3080 3085
Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
3090 3095 3100
Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
3105 3110 3115 312
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
3125 3130 3135
Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
3140 3145 3150
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
3155 3160 3165
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
3170 3175 3180
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
3185 3190 3195 320
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
3205 3210 3215
Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
3220 3225 3230
Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
3235 3240 3245
Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
3250 3255 3260
Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
3265 3270 3275 328
Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
3285 3290 3295
Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
3300 3305 3310
Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
3315 3320 3325
Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
3330 3335 3340
Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
3345 3350 3355 336
Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser
3365 3370 3375
Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys
3380 3385 3390
Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
3395 3400 3405
Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile
3410 3415

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10485 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 229...10482
 (D) OTHER INFORMATION: BRCA2 (OMI5)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC	60
TCTGCTGCGC CTCGGGTGTC TTTTGGCGCG GTGGGTGCGC GCCGGGAGAA GCGTGAGGGG	120
ACAGATTTGT GACCGGCGCG GTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT	180
CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT	237
Met Pro Ile	
1	
GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC	285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys	
5 10 15	
AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT	333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu	
20 25 30 35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA	381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
40 45 50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
55 60 65	
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	
70 75 80	
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT	525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	
85 90 95	
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA	573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	
100 105 110 115	
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC	621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	
120 125 130	
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
135 140 145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717

Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
150 155 160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
165 170 175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
180 185 190 195	
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
200 205 210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
215 220 225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005
Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg	
245 250 255	
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA	1053
Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys	
260 265 270 275	
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA CAT GTC CTA	1101
Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro His Val Leu	
280 285 290	
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT	1149
Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser	
295 300 305	
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA	1197
Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val	
310 315 320	
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT	1245
Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp	
325 330 335	
GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA	1293
Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val	
340 345 350 355	
TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA	1341
Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala	
360 365 370	
CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT	1389
His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val	

375										380					385					
GTA	CCG	TCT	TTG	GCC	TGT	GAA	TGG	TCT	CAA	CTA	ACC	CTT	TCA	GGT	CTA	1437				
Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu	Ser	Gly	Leu					
		390					395					400								
AAT	GGA	GCC	CAG	ATG	GAG	AAA	ATA	CCC	CTA	TTG	CAT	ATT	TCT	TCA	TGT	1485				
Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile	Ser	Ser	Cys					
	405					410					415									
GAC	CAA	AAT	ATT	TCA	GAA	AAA	GAC	CTA	TTA	GAC	ACA	GAG	AAC	AAA	AGA	1533				
Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu	Asn	Lys	Arg					
	420				425				430						435					
AAG	AAA	GAT	TTT	CTT	ACT	TCA	GAG	AAT	TCT	TTG	CCA	CGT	ATT	TCT	AGC	1581				
Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg	Ile	Ser	Ser					
			440					445					450							
CTA	CCA	AAA	TCG	GAG	AAG	CCA	TTA	AAT	GAG	GAA	ACA	GTG	GTA	AAT	AAG	1629				
Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val	Val	Asn	Lys					
			455				460						465							
AGA	GAT	GAA	GAG	CAG	CAT	CTT	GAA	TCT	CAT	ACA	GAC	TGC	ATT	CTT	GCA	1677				
Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys	Ile	Leu	Ala					
	470					475					480									
GTA	AAG	CAG	GCA	ATA	TCT	GGA	ACT	TCT	CCA	GTG	GCT	TCT	TCA	TTT	CAG	1725				
Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser	Ser	Phe	Gln					
	485					490					495									
GGT	ATC	AAA	AAG	TCT	ATA	TTC	AGA	ATA	AGA	GAA	TCA	CCT	AAA	GAG	ACT	1773				
Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro	Lys	Glu	Thr					
	500				505					510					515					
TTC	AAT	GCA	AGT	TTT	TCA	GGT	CAT	ATG	ACT	GAT	CCA	AAC	TTT	AAA	AAA	1821				
Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn	Phe	Lys	Lys					
			520					525						530						
GAA	ACT	GAA	GCC	TCT	GAA	AGT	GGA	CTG	GAA	ATA	CAT	ACT	GTT	TGC	TCA	1869				
Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr	Val	Cys	Ser					
			535					540					545							
CAG	AAG	GAG	GAC	TCC	TTA	TGT	CCA	AAT	TTA	ATT	GAT	AAT	GGA	AGC	TGG	1917				
Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn	Gly	Ser	Trp					
		550					555					560								
CCA	GCC	ACC	ACC	ACA	CAG	AAT	TCT	GTA	GCT	TTG	AAG	AAT	GCA	GGT	TTA	1965				
Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn	Ala	Gly	Leu					
		565				570					575									
ATA	TCC	ACT	TTG	AAA	AAG	AAA	ACA	AAT	AAG	TTT	ATT	TAT	GCT	ATA	CAT	2013				
Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr	Ala	Ile	His					
	580				585					590					595					
GAT	GAA	ACA	TCT	TAT	AAA	GGA	AAA	AAA	ATA	CCG	AAA	GAC	CAA	AAA	TCA	2061				
Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp	Gln	Lys	Ser					
				600					605						610					

GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA	2109
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala	
615 620 625	
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG	2157
Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val	
630 635 640	
AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA	2205
Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu	
645 650 655	
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA	2253
Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr	
660 665 670 675	
TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA	2301
Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala	
680 685 690	
AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT	2349
Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp	
695 700 705	
TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC	2397
Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser	
710 715 720	
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC	2445
Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His	
725 730 735	
CCA GTA CAA CAC TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC	2493
Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser	
740 745 750 755	
CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA	2541
Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu	
760 765 770	
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA	2589
Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg	
775 780 785	
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT	2637
Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr	
790 795 800	
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA	2685
Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln	
805 810 815	
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA	2733
Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro	
820 825 830 835	

CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC	2781
Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe	
840 845 850	
AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT	2829
Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr	
855 860 865	
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC	2877
Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe	
870 875 880	
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA ATA GCT AAT GAA AGG AAT	2925
Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Ile Ala Asn Glu Arg Asn	
885 890 895	
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT	2973
Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr	
900 905 910 915	
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA	3021
Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly	
920 925 930	
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG	3069
Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu	
935 940 945	
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA	3117
Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile	
950 955 960	
AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA	3165
Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile	
965 970 975	
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG GAC AAA TGG GCA GGA	3213
Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys Trp Ala Gly	
980 985 990 995	
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA	3261
Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr	
1000 1005 1010	
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC	3309
Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser	
1015 1020 1025	
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT	3357
Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala	
1030 1035 1040	
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG	3405
Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu	
1045 1050 1055	
AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT	3453

1285	1290	1295	
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg 1300 1305 1310 1315			4173
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser 1320 1325 1330			4221
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val 1335 1340 1345			4269
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn 1350 1355 1360			4317
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln 1365 1370 1375			4365
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala 1380 1385 1390 1395			4413
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala 1400 1405 1410			4461
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe 1415 1420 1425			4509
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe 1430 1435 1440			4557
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn 1445 1450 1455			4605
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met 1460 1465 1470 1475			4653
GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu 1480 1485 1490			4701
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln 1495 1500 1505			4749
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly 1510 1515 1520			4797

TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG	4845
Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu	
1525 1530 1535	
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA	4893
Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu	
1540 1545 1550 1555	
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG	4941
Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu	
1560 1565 1570	
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT	4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala	
1575 1580 1585	
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC	5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn	
1590 1595 1600	
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT	5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn	
1605 1610 1615	
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG	5133
Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu	
1620 1625 1630 1635	
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT	5181
Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro	
1640 1645 1650	
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA	5229
Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser	
1655 1660 1665	
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG	5277
Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln	
1670 1675 1680	
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT	5325
Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp	
1685 1690 1695	
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG	5373
Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu	
1700 1705 1710 1715	
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT	5421
Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His	
1720 1725 1730	
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC	5469
Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn	
1735 1740 1745	

AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu 1750 1755 1760	5517
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val 1765 1770 1775	5565
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys 1780 1785 1790 1795	5613
GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu 1800 1805 1810	5661
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile 1815 1820 1825	5709
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala 1830 1835 1840	5757
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile 1845 1850 1855	5805
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys 1860 1865 1870 1875	5853
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala 1880 1885 1890	5901
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser 1895 1900 1905	5949
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp 1910 1915 1920	5997
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu 1925 1930 1935	6045
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser 1940 1945 1950 1955	6093
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser 1960 1965 1970	6141
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG	6189

Ala Asn Thr Cys Gly Ile Phe Ser Thr	Ala Ser Gly Lys Ser Val Gln	
1975	1980	1985
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA	6237	
Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile		
1990	1995	2000
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC	6285	
Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn		
2005	2010	2015
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT	6333	
Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr		
2020	2025	2030
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT	6381	
Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn		
2040	2045	2050
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC	6429	
Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser		
2055	2060	2065
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT	6477	
Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe		
2070	2075	2080
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA	6525	
Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg		
2085	2090	2095
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG	6573	
Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu		
2100	2105	2110
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA	6621	
His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys		
2120	2125	2130
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC	6669	
Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His		
2135	2140	2145
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA	6717	
Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln		
2150	2155	2160
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT	6765	
Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val		
2165	2170	2175
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT	6813	
Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly		
2180	2185	2190
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT	6861	
Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val		

2200	2205	2210	
TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala 2215 2220 2225			6909
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser 2230 2235 2240			6957
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn 2245 2250 2255			7005
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu 2260 2265 2270 2275			7053
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn 2280 2285 2290			7101
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser 2295 2300 2305			7149
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His 2310 2315 2320			7197
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys 2325 2330 2335			7245
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu 2340 2345 2350 2355			7293
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser 2360 2365 2370			7341
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala 2375 2380 2385			7389
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr 2390 2395 2400			7437
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val 2405 2410 2415			7485
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln 2420 2425 2430 2435			7533

AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC 7581
Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp
2440 2445 2450

AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT 7629
Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala
2455 2460 2465

GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT 7677
Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser
2470 2475 2480

CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA 7725
Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln
2485 2490 2495

AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA 7773
Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr
2500 2505 2510 2515

TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT 7821
Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val
2520 2525 2530

CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA 7869
Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys
2535 2540 2545

CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC 7917
His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His
2550 2555 2560

ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA 7965
Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile
2565 2570 2575

CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT 8013
Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala
2580 2585 2590 2595

GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT 8061
Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp
2600 2605 2610

CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC 8109
Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile
2615 2620 2625

ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT 8157
Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala
2630 2635 2640

AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA 8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg
2645 2650 2655

TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA 8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile
2660 2665 2670 2675

ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT 8301
Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser
2680 2685 2690

GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA 8349
Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys
2695 2700 2705

ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT 8397
Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp
2710 2715 2720

GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC 8445
Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val
2725 2730 2735

TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA 8493
Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly
2740 2745 2750 2755

GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA 8541
Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro
2760 2765 2770

GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC 8589
Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg
2775 2780 2785

TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG 8637
Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu
2790 2795 2800

CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT 8685
Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp
2805 2810 2815

GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA 8733
Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser
2820 2825 2830 2835

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA 8781
Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala
2840 2845 2850

GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT 8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr
2855 2860 2865

AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA 8877
Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro
2870 2875 2880

TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA 8925

Tyr	Leu	Pro	Ser	Arg	Ala	Leu	Thr	Arg	Gln	Gln	Val	Arg	Ala	Leu	Gln		
2885						2890					2895						
GAT	GGT	GCA	GAG	CTT	TAT	GAA	GCA	GTG	AAG	AAT	GCA	GCA	GAC	CCA	GCT	8973	
Asp	Gly	Ala	Glu	Leu	Tyr	Glu	Ala	Val	Lys	Asn	Ala	Ala	Asp	Pro	Ala		
2900				2905					2910						2915		
TAC	CTT	GAG	GGT	TAT	TTC	AGT	GAA	GAG	CAG	TTA	AGA	GCC	TTG	AAT	AAT	9021	
Tyr	Leu	Glu	Gly	Tyr	Phe	Ser	Glu	Glu	Gln	Leu	Arg	Ala	Leu	Asn	Asn		
				2920					2925					2930			
CAC	AGG	CAA	ATG	TTG	AAT	GAT	AAG	AAA	CAA	GCT	CAG	ATC	CAG	TTG	GAA	9069	
His	Arg	Gln	Met	Leu	Asn	Asp	Lys	Lys	Gln	Ala	Gln	Ile	Gln	Leu	Glu		
			2935					2940					2945				
ATT	AGG	AAG	ACC	ATG	GAA	TCT	GCT	GAA	CAA	AAG	GAA	CAA	GGT	TTA	TCA	9117	
Ile	Arg	Lys	Thr	Met	Glu	Ser	Ala	Glu	Gln	Lys	Glu	Gln	Gly	Leu	Ser		
		2950					2955					2960					
AGG	GAT	GTC	ACA	ACC	GTG	TGG	AAG	TTG	CGT	ATT	GTA	AGC	TAT	TCA	AAA	9165	
Arg	Asp	Val	Thr	Thr	Val	Trp	Lys	Leu	Arg	Ile	Val	Ser	Tyr	Ser	Lys		
	2965					2970					2975						
AAA	GAA	AAA	GAT	TCA	GTT	ATA	CTG	AGT	ATT	TGG	CGT	CCA	TCA	TCA	GAT	9213	
Lys	Glu	Lys	Asp	Ser	Val	Ile	Leu	Ser	Ile	Trp	Arg	Pro	Ser	Ser	Asp		
2980				2985					2990						2995		
TTA	TAT	TCT	CTG	TTA	ACA	GAA	GGA	AAG	AGA	TAC	AGA	ATT	TAT	CAT	CTT	9261	
Leu	Tyr	Ser	Leu	Leu	Thr	Glu	Gly	Lys	Arg	Tyr	Arg	Ile	Tyr	His	Leu		
			3000					3005						3010			
GCA	ACT	TCA	AAA	TCT	AAA	AGT	AAA	TCT	GAA	AGA	GCT	AAC	ATA	CAG	TTA	9309	
Ala	Thr	Ser	Lys	Ser	Lys	Ser	Lys	Ser	Glu	Arg	Ala	Asn	Ile	Gln	Leu		
		3015					3020					3025					
GCA	GCG	ACA	AAA	AAA	ACT	CAG	TAT	CAA	CAA	CTA	CCG	GTT	TCA	GAT	GAA	9357	
Ala	Ala	Thr	Lys	Lys	Thr	Gln	Tyr	Gln	Gln	Leu	Pro	Val	Ser	Asp	Glu		
		3030				3035					3040						
ATT	TTA	TTT	CAG	ATT	TAC	CAG	CCA	CGG	GAG	CCC	CTT	CAC	TTC	AGC	AAA	9405	
Ile	Leu	Phe	Gln	Ile	Tyr	Gln	Pro	Arg	Glu	Pro	Leu	His	Phe	Ser	Lys		
	3045				3050					3055							
TTT	TTA	GAT	CCA	GAC	TTT	CAG	CCA	TCT	TGT	TCT	GAG	GTG	GAC	CTA	ATA	9453	
Phe	Leu	Asp	Pro	Asp	Phe	Gln	Pro	Ser	Cys	Ser	Glu	Val	Asp	Leu	Ile		
3060				3065					3070					3075			
GGA	TTT	GTC	GTT	TCT	GTT	GTG	AAA	AAA	ACA	GGA	CTT	GCC	CCT	TTC	GTC	9501	
Gly	Phe	Val	Val	Ser	Val	Val	Lys	Lys	Thr	Gly	Leu	Ala	Pro				

3110	3115	3120	
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe 3125 3130 3135			9645
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe 3140 3145 3150 3155			9693
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile 3160 3165 3170			9741
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn 3175 3180 3185			9789
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr 3190 3195 3200			9837
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser 3205 3210 3215			9885
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala 3220 3225 3230 3235			9933
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys 3240 3245 3250			9981
TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys 3255 3260 3265			10029
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Val 3270 3275 3280			10077
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln 3285 3290 3295			10125
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys 3300 3305 3310 3315			10173
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile 3320 3325 3330			10221
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile 3335 3340 3345			10269

AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA	10317
Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile	
3350 3355 3360	
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT	10365
Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr	
3365 3370 3375	
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG	10413
Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu	
3380 3385 3390 3395	
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA	10461
Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr	
3400 3405 3410	
ATT ACA ACT AAA AAA TAT ATC TAA	10485
Ile Thr Thr Lys Lys Tyr Ile	
3415	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Pro	Ile	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys
1				5					10					15	
Thr	Arg	Cys	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe
			20					25					30		
Glu	Glu	Leu	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu
		35					40					45			
Glu	Ser	Glu	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr
	50				55						60				
Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile
65					70				75					80	
Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys
				85				90						95	
Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser
			100					105					110		
Arg	His	Lys	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp
		115					120					125			
Asp	Val	Ser	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val
		130				135					140				
Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val
145					150				155					160	
Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr
				165					170					175	

Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
 180 185 190
 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
 195 200 205
 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
 210 215 220
 Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
 225 230 235 240
 Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
 245 250 255
 Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
 260 265 270
 Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
 275 280 285
 His Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
 290 295 300
 Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
 305 310 315 320
 Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
 325 330 335
 Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
 340 345 350
 Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
 355 360 365
 Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
 370 375 380
 Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
 385 390 395 400
 Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
 405 410 415
 Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
 420 425 430
 Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
 435 440 445
 Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
 450 455 460
 Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
 465 470 475 480
 Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
 485 490 495
 Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
 500 505 510
 Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
 515 520 525
 Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
 530 535 540
 Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
 545 550 555 560
 Gly Ser Trp Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
 565 570 575
 Ala Gly Leu Ile Ser Thr Leu Lys Lys Thr Asn Lys Phe Ile Tyr
 580 585 590
 Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
 595 600 605
 Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
 610 615 620
 Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His

625					630					635					640
Ser	Ser	Val	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr
				645					650					655	
Leu	Ser	Leu	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg
			660					665					670		
Asn	Glu	Thr	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr
		675					680					685			
Lys	Glu	Ala	Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro
	690					695				700					
Glu	Ala	Asp	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp
705					710				715					720	
Pro	Lys	Ser	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala
			725					730					735		
Ala	Cys	His	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp
		740						745					750		
Phe	Gln	Ser	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr
		755					760					765			
Leu	Ile	Leu	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met
	770					775					780				
Ile	Ser	Arg	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly
785					790					795				800	
Asn	Asn	Tyr	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu
				805				810					815		
Lys	Asn	Gln	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu
		820						825				830			
Leu	Leu	Pro	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys
		835					840					845			
Val	Gln	Phe	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln
	850					855				860					
Glu	Glu	Thr	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu
865					870				875					880	
Glu	Leu	Phe	Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Ile	Ala	Asn
				885				890					895		
Glu	Arg	Asn	Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His	Glu	Thr
			900					905					910		
Asp	Leu	Thr	Cys	Val	Asn	Glu	Pro	Ile	Phe	Lys	Asn	Ser	Thr	Met	Val
		915					920					925			
Leu	Tyr	Gly	Asp	Thr	Gly	Asp	Lys	Gln	Ala	Thr	Gln	Val	Ser	Ile	Lys
	930					935				940					
Lys	Asp	Leu	Val	Tyr	Val	Leu	Ala	Glu	Glu	Asn	Lys	Asn	Ser	Val	Lys
945					950				955					960	
Gln	His	Ile	Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp	Ile	Ser
			965					970					975		
Leu	Asn	Ile	Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asp	Lys
		980						985					990		
Trp	Ala	Gly	Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser
	995					1000						1005			
Phe	Arg	Thr	Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile
	1010					1015						1020			
Lys	Lys	Ser	Lys	Met	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr	
1025					1030				1035					104	
Ser	Leu	Ala	Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu	Asp	Asn	Gln
			1045					1050					1055		
Lys	Lys	Leu	Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val	Ser	Ala	His	Leu
		1060						1065					1070		
Gln	Ser	Ser	Val	Val	Val	Ser	Asp	Cys	Lys	Asn	Ser	His	Ile	Thr	Pro
		1075					1080					1085			

Gln Met Leu Phe Ser Lys	Gln Asp Phe Asn Ser	Asn His Asn Leu Thr
1090	1095	1100
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu		
1105	1110	1115
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile		
1125	1130	1135
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu		
1140	1145	1150
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met		
1155	1160	1165
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly		
1170	1175	1180
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys		
1185	1190	1195
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe		
1205	1210	1215
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu		
1220	1225	1230
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser		
1235	1240	1245
Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys		
1250	1255	1260
Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp		
1265	1270	1275
Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn		
1285	1290	1295
Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn		
1300	1305	1310
Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser		
1315	1320	1325
Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn		
1330	1335	1340
Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp		
1345	1350	1355
Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly		
1365	1370	1375
Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val		
1380	1385	1390
Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln		
1395	1400	1405
Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser		
1410	1415	1420
Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys		
1425	1430	1435
Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu		
1445	1450	1455
Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys		
1460	1465	1470
Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His		
1475	1480	1485
Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val		
1490	1495	1500
Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr		
1505	1510	1515
Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys		
1525	1530	1535
Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly		

			1540					1545					1550			
Thr	Ser	Glu	Ile	Thr	Ser	Phe	Ser	His	Gln	Trp	Ala	Lys	Thr	Leu	Lys	
		1555					1560					1565				
Tyr	Arg	Glu	Ala	Cys	Lys	Asp	Leu	Glu	Leu	Ala	Cys	Glu	Thr	Ile	Glu	
	1570					1575					1580					
Ile	Thr	Ala	Ala	Pro	Lys	Cys	Lys	Glu	Met	Gln	Asn	Ser	Leu	Asn	Asn	
1585					1590					1595						160
Asp	Lys	Asn	Leu	Val	Ser	Ile	Glu	Thr	Val	Val	Pro	Pro	Lys	Leu	Leu	
				1605					1610					1615		
Ser	Asp	Asn	Leu	Cys	Arg	Gln	Thr	Glu	Asn	Leu	Lys	Thr	Ser	Lys	Ser	
			1620					1625					1630			
Ile	Phe	Leu	Lys	Val	Lys	Val	His	Glu	Asn	Val	Glu	Lys	Glu	Thr	Ala	
	1635					1640					1645					
Lys	Ser	Pro	Ala	Thr	Cys	Tyr	Thr	Asn	Gln	Ser	Pro	Tyr	Ser	Val	Ile	
	1650					1655					1660					
Glu	Asn	Ser	Ala	Leu	Ala	Phe	Tyr	Thr	Ser	Cys	Ser	Arg	Lys	Thr	Ser	
1665					1670					1675						168
Val	Ser	Gln	Thr	Ser	Leu	Leu	Glu	Ala	Lys	Lys	Trp	Leu	Arg	Glu	Gly	
				1685					1690					1695		
Ile	Phe	Asp	Gly	Gln	Pro	Glu	Arg	Ile	Asn	Thr	Ala	Asp	Tyr	Val	Gly	
	1700					1705					1710					
Asn	Tyr	Leu	Tyr	Glu	Asn	Asn	Ser	Asn	Ser	Thr	Ile	Ala	Glu	Asn	Asp	
	1715					1720					1725					
Lys	Asn	His	Leu	Ser	Glu	Lys	Gln	Asp	Thr	Tyr	Leu	Ser	Asn	Ser	Ser	
	1730					1735					1740					
Met	Ser	Asn	Ser	Tyr	Ser	Tyr	His	Ser	Asp	Glu	Val	Tyr	Asn	Asp	Ser	
1745					1750					1755						176
Gly	Tyr	Leu	Ser	Lys	Asn	Lys	Leu	Asp	Ser	Gly	Ile	Glu	Pro	Val	Leu	
			1765					1770					1775			
Lys	Asn	Val	Glu	Asp	Gln	Lys	Asn	Thr	Ser	Phe	Ser	Lys	Val	Ile	Ser	
	1780					1785					1790					
Asn	Val	Lys	Asp	Ala	Asn	Ala	Tyr	Pro	Gln	Thr	Val	Asn	Glu	Asp	Ile	
	1795					1800					1805					
Cys	Val	Glu	Glu	Leu	Val	Thr	Ser	Ser	Ser	Pro	Cys	Lys	Asn	Lys	Asn	
	1810					1815					1820					
Ala	Ala	Ile	Lys	Leu	Ser	Ile	Ser	Asn	Ser	Asn	Asn	Phe	Glu	Val	Gly	
1825					1830					1835						184
Pro	Pro	Ala	Phe	Arg	Ile	Ala	Ser	Gly	Lys	Ile	Val	Cys	Val	Ser	His	
			1845					1850					1855			
Glu	Thr	Ile	Lys	Lys	Val	Lys	Asp	Ile	Phe	Thr	Asp	Ser	Phe	Ser	Lys	
		1860					1865					1870				
Val	Ile	Lys	Glu	Asn	Asn	Glu	Asn	Lys	Ser	Lys	Ile	Cys	Gln	Thr	Lys	
	1875					1880					1885					
Ile	Met	Ala	Gly	Cys	Tyr	Glu	Ala	Leu	Asp	Asp	Ser	Glu	Asp	Ile	Leu	
	1890					1895					1900					
His	Asn	Ser	Leu	Asp	Asn	Asp	Glu	Cys	Ser	Thr	His	Ser	His	Lys	Val	
1905					1910					1915						192
Phe	Ala	Asp	Ile	Gln	Ser	Glu	Glu	Ile	Leu	Gln	His	Asn	Gln	Asn	Met	
			1925					1930					1935			
Ser	Gly	Leu	Glu	Lys	Val	Ser	Lys	Ile	Ser	Pro	Cys	Asp	Val	Ser	Leu	

Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
 2005 2010 2015
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
 2020 2025 2030
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
 2035 2040 2045
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
 2050 2055 2060
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
 2065 2070 2075 208
 Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
 2085 2090 2095
 Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
 2100 2105 2110
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
 2115 2120 2125
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
 2130 2135 2140
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
 2145 2150 2155 216
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
 2165 2170 2175
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
 2180 2185 2190
 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
 2195 2200 2205
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
 2210 2215 2220
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
 2225 2230 2235 224
 Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
 2245 2250 2255
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
 2260 2265 2270
 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
 2275 2280 2285
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
 2290 2295 2300
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
 2305 2310 2315 232
 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
 2325 2330 2335
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
 2340 2345 2350
 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
 2355 2360 2365
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
 2370 2375 2380
 Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
 2385 2390 2395 240
 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
 2405 2410 2415
 His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
 2420 2425 2430
 Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
 2435 2440 2445
 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln

2450	2455	2460
Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu		
2465	2470	2475
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys		248
	2485	2490
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu		2495
	2500	2505
Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly		2510
	2515	2520
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly		2525
	2530	2535
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe		2540
2545	2550	2555
Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly		256
	2565	2570
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp		2575
	2580	2585
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro		2590
	2595	2600
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr		2605
	2610	2615
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys		2620
2625	2630	2635
Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu		264
	2645	2650
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile		2655
	2660	2665
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu		2670
	2675	2680
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser		2685
	2690	2695
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu		2700
2705	2710	2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu		272
	2725	2730
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile		2735
	2740	2745
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu		2750
	2755	2760
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg		2765
	2770	2775
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro		2780
2785	2790	2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly		280
	2805	2810
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu		2815
	2820	2825
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu		2830
	2835	2840
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala		2845
	2850	2855
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr		2860
2865	2870	2875
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg		288
	2885	2890
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala		2895
	2900	2905
		2910

Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
 2915 2920 2925
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
 2930 2935 2940
 Gln Leu Glu Ile Arg Lys Thr Met Glu Ser Ala Glu Gln Lys Glu Gln
 2945 2950 2955 296
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
 2965 2970 2975
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
 2980 2985 2990
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
 2995 3000 3005
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
 3010 3015 3020
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
 3025 3030 3035 304
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
 3045 3050 3055
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
 3060 3065 3070
 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
 3075 3080 3085
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
 3090 3095 3100
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
 3105 3110 3115 312
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
 3125 3130 3135
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
 3140 3145 3150
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
 3155 3160 3165
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
 3170 3175 3180
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
 3185 3190 3195 320
 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
 3205 3210 3215
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
 3220 3225 3230
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
 3235 3240 3245
 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
 3250 3255 3260
 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
 3265 3270 3275 328
 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
 3285 3290 3295
 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
 3300 3305 3310
 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
 3315 3320 3325
 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
 3330 3335 3340
 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
 3345 3350 3355 336
 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser

	3365		3370		3375
Glu Asp Tyr	Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys				
	3380		3385		3390
Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys					
	3395		3400		3405
Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile					
	3410		3415		

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGAGTTTTAC CTCAGTCACA

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CAGGAAACAG CTATGACCCT GTGACGTACT GGGTTTTTAC C

41

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 3FII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCTTTAAC TGTTCTGGGT CACA

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 3RII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCAGCATGA CACAATTAAT GA

22

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...44
- (D) OTHER INFORMATION: 4F/M 13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGTAAAACGA CGGCCAGTAG AATGCAAATT TATAATCCAG AGTA

44

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 4R-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATCAGATTCA TCTTTATAGA AC

22

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 5+6F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGTAAAACGA CGGCCAGTTG TGTTGGCATT TTAAACATCA

40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 5+6R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGGAAACAG CTATGACCCA GGGCAAAGGT ATAACGCT

38

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38

(D) OTHER INFORMATION: 7F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGTAAAACGA CGGCCAGTTA AGTGAAATAA AGAGTGAA

38

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...36
- (D) OTHER INFORMATION: 7R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAGGAAACAG CTATGACCAG AAGTATTAGA GATGAC

36

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 8F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGTAAAACGA CGGCCAGTGC CATATCTTAC CACCTTGTGA

40

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: other

- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 8FIA primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTGCATTCTA GTGATAATAT AC

22

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 8RIA primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AATTGTTAGC AATTTCAAC

19

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 9F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGTAAAACGA CGGCCAGTTG GACCTAGGTT GATTGCAGAT

40

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE
 - (A) NAME/KEY: other
 - (B) LOCATION: 1...40
 - (D) OTHER INFORMATION: 9R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAGGAAACAG CTATGACCTA AACTGAGATC ACGGGTGACA

40

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...24
- (D) OTHER INFORMATION: 10AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATAATATA AATTATATGG CTTA

24

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 10AR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAGGAAACAG CTATGACCCC TAGTCTTGCT AGTTCTT

37

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...42

(D) OTHER INFORMATION: 10BF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGTAAAACGA CGGCCAGTAR CTGAAGTGA ACCAAATGAT AC

42

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...44

(D) OTHER INFORMATION: 10BR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGGAAACAG CTATGACCAC GTGGCAAAGA ATTCTCTGAA GTAA

44

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(ii) MOLECULE TYPE: Genomic DNA

(A) NAME/KEY: other

(B) LOCATION: 1...40

(D) OTHER INFORMATION: 10CF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TGTAAAACGA CGGCCAGTCA GCATCTTGAA TCTCATACAG

40

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 10CRII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGACAGAGGT ACCTGAATC

19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 11AF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGTAAAACGA CGGCCAGTTG GTACTTTAAT TTTGTCACTT

40

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 11AR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGGAAACAG CTATGACCTG CAGGCATGAC AGAGAAT

37

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11BF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAGAAGCAAA ATGTAATAAG GA

22

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11BR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CATTTAAAGC ACATACATCT TG

22

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: primer
- (B) LOCATION:
- (D) OTHER INFORMATION: 11CF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCTAGAGGCA AAGAATCATA C

21

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11CR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CAAGATTATT CCTTTCATTA GC

22

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11DF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AACCAAAACA CAAATCTAAG AG

22

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11DR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTCATTTTTA TATGCTGCTT TAC

23

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11EF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGTTTTATAT GGAGACACAG G

21

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11ER primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTATTACAA TTTCAACACA AGC

23

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11FF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATCACAGTTT TGGAGGTAGC

20

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11FR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTGACTTCCT GATTCTTCTA A

21

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11GF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTCAGATGTT ATTTTCCAAG C

21

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11GR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGTTAAATA ACCAGAAGCA C

21

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...18
- (D) OTHER INFORMATION: 11HF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGGTAGACAG CAGCAAGC

18

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11HR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTAATATCAG TTGGCATTTA TT

22

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11IF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TGCAGAGGTA CATCCAATAA G

21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11IR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCAGTAAA TAGCAAGTCC G

21

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11JF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TACTGAAAAT GAAGATAACA AAT

23

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11JR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATTTTGTTCT TTCTTATGTC AG

22

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11KF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA

35

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11KR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG

35

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11LF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CACAAAATAC TGAAAGAAAG TG

22

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 11LR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGCACCACAG TCTCAATAG

19

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11MF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCAAAGACCC TAAAGTACAG

20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other
(B) LOCATION: 1...22
(D) OTHER INFORMATION: 11MR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CATCAAATAT TCCTTCTCTA AG 22

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other
(B) LOCATION: 1...35
(D) OTHER INFORMATION: 11NF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGTAAAACGA CGGCCAGTGA AAATTCAGCC TTAGC 35

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other
(B) LOCATION: 1...35
(D) OTHER INFORMATION: 11NR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CAGGAAACAG CTATGACCAT CAGAATGGTA GGAAT 35

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 110F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTACTATAGC TGAAAATGAC AA

22

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 110R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCACTGGCT ATCCTAAATG

20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11PF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TGAAGATATT TGC GTTGAGG

20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11PR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTCAGCAAAA ACCTTATGTG

20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11QF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACGAAAATTA TGGCAGGTTG T

21

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11QR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTTGTCTTGC GTTTTGTAAT G

21

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11RF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GCTTCATAAG TCACTCTCAT

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11RR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCAAATTCCT CTAACACTCC

20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other

- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11SF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TGTAAAACGA CGGCCAGTTA CAGCAAGTGG AAAGC

35

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 11SR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CAGGAAACAG CTATGACCAA GTTTCAGTTT TACCAAT

37

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11TF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTTCTTCAGA AAATAATCAC TC

22

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11TR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TGTAAAAAGA GAATGTGTGG C

21

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 11UF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTAAACGA CGGCCAGTAC TTTTCTGAT GTTCCTGTG

39

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 11UR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CAGGAAACAG CTATGACCTA AAAATAGTGA TTGGCAACA

39

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...42
- (D) OTHER INFORMATION: 12F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TGTAAAACGA CGGCCAGTAG TGGTGTTTTA AAGTGGTCAA AA

42

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 12R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAGGAAACAG CTATGACCGG ATCCACCTGA GGTCAGAATA

40

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 13-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TAACATTTTAA GCATCCGTTA C

21

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...28
- (D) OTHER INFORMATION: 13-2R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AAACGAGACT TTTCTCATAC TGTATTAG

28

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 14F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ACCATGTAGC AAATGAGGGT CT

22

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 14AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GCTTTTGTCT GTTTTCCTCC AA

22

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 15-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCAGGGGTTG TGCTTTTAA A

21

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: primer
- (B) LOCATION:
- (D) OTHER INFORMATION: 15FUT/M13-R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAGGAAACAG CTATGACCAC TCTGTCATAA AAGCCATC

38

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...24
- (D) OTHER INFORMATION: 16AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTTGTTTGT TATAATTGTT TTTA

24

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 16AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CCAACTTTTT AGTTCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 17F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TTCAGTATCA TCCTATGTG

19

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other

- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 17AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGAAACCTTA ACCCATACTG

20

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 18FUT/M13-AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TGTAAAACGA CGGCCAGTGA ATTCTAGAGT CACACTTCC

39

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 18R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAGGAAACAG CTATGACCTT TAACTGAATC AATGACTG

38

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...41
- (D) OTHER INFORMATION: 19F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TGTAAAACGA CGGCCAGTAA GTGAATATTT TTAAGGCAGT T

41

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 19FUT/M13-R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CAGGAAACAG CTATGACCAA GAGACCGAAA CTCCATCTC

39

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 20F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGTAAAACGA CGGCCAGTCA CTGTGCCTGG CCTGATAC

38

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...39

(D) OTHER INFORMATION: 20R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CAGGAAACAG CTATGACCAT GTTAAATTCA AAGTCTCTA

39

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...39

(D) OTHER INFORMATION: 21F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TGTAAAACGA CGGCCAGTGG GTGTTTTATG CTTGGTTCT

39

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...40

(D) OTHER INFORMATION: 21R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CAGGAAACAG CTATGACCCA TTTCAACATA TTCCTTCCTG

40

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 22F-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AACCACACCC TTAAGATGA

19

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 22R-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCATTAGTAG TGGATTTTGC

20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...16
- (D) OTHER INFORMATION: 23FII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCACTTCCAT TGCATC

16

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...17
- (D) OTHER INFORMATION: 23RII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TGCCCAACTGG TAGCTCC

17

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 24 2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TACAGTTAGC AGCGACAAAA

20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 24R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:
CAGGAAACAG CTATGACCAT TTGCCAACTG GTAGCTCC

38

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 25F-7/23 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:
GCTTTCGCCA AATTCAGCTA

20

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 25R-7/23 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:
TACCAAAATG TGTGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 26-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AATCACTGAT ACTGGTTTTG

20

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 26-2R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TATACTTACA GGAGCCACAT

20

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...18
- (D) OTHER INFORMATION: 27AF-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTGTGTGTAA TATTTGCC

18

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...40

(D) OTHER INFORMATION: 27AR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CAGGAAACAG CTATGACGGC AAGTTCTTCG TCAGCTATTG

40

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...40

(D) OTHER INFORMATION: 27BF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TGTAAAACGA CGGCCAGTGA ATTCTCCTCA GATGACTCCA

40

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...38

(D) OTHER INFORMATION: 27BR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CAGGAAACAG CTATGACCTC TTTGCTCATT GTGCAACA

38